

STIC-Biotech/ChemLib

131954

From: Whiteman, Brian  
Sent: Wednesday, September 08, 2004 12:54 PM  
To: STIC-Biotech/ChemLib  
Subject: seq search

09/729,264 Welcher et al., 11/28/00

Please perform an olimoger search againts SEQ ID NOs: 1, 3 and 5.

If possible limit search to at least 16 nucleotides or more.

Thank you,

Brian Whiteman  
Remsen, 2D14  
mail box 2C18  
Patent Examiner - Art Unit 1635  
United States Patent and Trademark Office  
(571) 272-0764

CREE

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: 9/13  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence :# \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 22:59:39 ; Search time 3446.95 Seconds  
(without alignments)  
10179.449 Million cell updates/sec

Title: US-09-729-264-1  
Perfect score: 1175  
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Scoring table: OLIGO NUC  
Gapop\_60.0, Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 55024014

Minimum DB seq length: 16

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST.\*

1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estim.\*  
4: em\_estmu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pin.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rod.\*  
26: em\_gss\_phg.\*  
27: em\_gss\_vrl.\*  
28: gb\_gss1.\*  
29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	614	52.3	1201	13 BX399881	BX399881 BX399881
2	498	42.4	1201	13 BX358190	BX358190 BX358190
3	453	38.6	517	13 BX370118	BX370118 BX370118
4	443	37.7	941	13 BX403420	BX403420 BX403420

5	328	27.9	970	13 BX370209	BX370209 BX370209
6	267	22.7	725	12 BG740428	BG740428 BG740428
7	226	19.2	1148	13 BX370210	BX370210 BX370210
8	149	12.7	216	12 BG206666	BG206666 RST26117
9	146	12.4	622	29 AG069679	AG069679 Pan trogl
10	146	12.4	677	29 AG107877	AG107877 Pan trogl
11	110	9.4	1201	13 BX358189	BX358189 BX358189
12	100	8.5	185	14 N47851	N47851 yw9sh05.r1
13	100	8.5	234	14 N93995	N93995 za6sf09.r1
14	76	6.5	525	28 AQ403719	AQ403719 HS 5049 A
15	63	5.4	976	14 CK230652	CK230652 ILLUMIGEN
16	51	4.3	457	9 AJ003343	AJ003343
17	51	4.3	554	14 CB128910	CB128910 K-EST0178
18	45	3.8	983	14 CK230612	CK230612 ILLUMIGEN
19	34	2.9	527	10 BE032610	BE032610 132035 MA
20	33	2.8	685	29 AG142221	AG142221 Pan trogl
21	27	2.3	565	14 CD344913	CD344913 EtEstee75
22	25	2.1	635	28 AQ541776	AQ541776 RPCI-11-3
23	24	2.0	68	29 AB082057	AB082057 Drosophi1
24	24	2.0	680	9 AA941851	AA941851 LD27161.5
25	23	2.0	219	13 BQ862485	BQ862485 QGC21D13.
26	23	2.0	291	28 AZ411779	AZ411779 IM0185B04
27	23	2.0	316	13 BQ864023	BQ864023 QGC2108.
28	23	2.0	631	10 BB663870	BB663870 BB663870
29	23	2.0	664	28 BH020641	BH020641 L8612a.d
30	23	2.0	773	14 CB648901	CB648901 OSJNB121
31	23	2.0	784	12 BG863468	BG863468 602796941
32	23	2.0	794	10 BF784177	BF784177 602108039
33	23	2.0	1510	11 AK086973	AK086973 Mus muscu
34	22	1.9	167	29 CG475380	CG475380 OST3669 M
35	22	1.9	171	29 CG480695	CG480695 OST12736
36	22	1.9	188	13 BQ134412	BQ134412 1091016H0
37	22	1.9	196	29 CG480560	CG480560 OST12523
38	22	1.9	219	29 CG479279	CG479279 OST9980 M
39	22	1.9	223	29 CG615044	CG615044 OST303854
40	22	1.9	232	29 CG481750	CG481750 OST14380
41	22	1.9	234	29 CG481764	CG481764 OST14399
42	22	1.9	238	29 CG566401	CG566401 OST192013
43	22	1.9	287	10 BB343618	BB343618 BB343618
44	22	1.9	328	29 CG476832	CG476832 OST6476 M
45	22	1.9	340	14 Z46691	Z46691 ATTS4353 Pe

#### ALIGNMENTS

RESULT 1  
BX399881  
LOCUS  
DEFINITION  
BX399881 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cdna  
clone CS0D1085YA24 5-PRIME, mRNA sequence.  
ACCESSION  
BX399881  
VERSION  
BX399881.1 GI:30622019  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1201)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 10299.f, and  
it belongs to a clone representative of this cluster. For more  
information about this cluster and the virtual cDNA, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0D1085BA120P1&cluster=10299.f. Contact :  
Peng Liang Email : fliang@lifetech.com URL :

BX399881 1201 bp mRNA linear EST 13-MAY-2003  
BX399881 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cdna  
clone CS0D1085YA24 5-PRIME, mRNA sequence.  
BX399881  
BX399881.1 GI:30622019  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1201)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 10299.f, and  
it belongs to a clone representative of this cluster. For more  
information about this cluster and the virtual cDNA, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0D1085BA120P1&cluster=10299.f. Contact :  
Peng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue  
Genoscope sequence ID : CS0DI085BA12QPI.

## FEATURES

source  
1. .1201  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="CS0DI085YA24"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo (dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 52.3%; Score 614; DB 13; Length 1201;  
Best Local Similarity 100.0%; Pred. No. 1.3e-295;  
Matches 614; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 52 GTTCTGGGTCTGTAATGAGTCATAGAGGCCGCCAGAAATCAACAGTCCTGAAGGGCT 111  
Db 272 GTTCTGGGTCTGTAATGAGTCATAGAGGCCGCCAGAAATCAACAGTCCTGAAGGGCT 331  
QY 112 CCCAGGCTCGCTTCAACTGCACCGCTCTCCAGGGCTGGAAGCTCATCATGTGGGCTCTCA 171  
Db 332 CCCAGGCTCGCTTCAACTGCACCGCTCTCCAGGGCTGGAAGCTCATCATGTGGGCTCTCA 391  
QY 172 GTGACATGTGTGTGTTAAGCGTCAAGCCCATGAGGCCCATCATCATCAATGACCGCTTCA 231  
Db 392 GTGACATGTGTGTGTTAAGCGTCAAGCCCATGAGGCCCATCATCATCAATGACCGCTTCA 451  
QY 232 CTTCTCAGAGTACGACGAGGGGGAACTTCACTCGGAGTATCATCCCAATGTCG 291  
Db 452 CTTCTCAGAGTACGACGAGGGGGAACTTCACTCGGAGTATCATCCCAATGTCG 511  
QY 292 AGCCAGTATTCGGGGAAACATCAGATGACGCTCCAGAACAGTCGCGCTGCATGATCTG 351  
Db 512 AGCCAGTATTCGGGGAAACATCAGATGACGCTCCAGAACAGTCGCGCTGCATGATCTG 571  
QY 352 CTTACCTTACCGTCCAAAGTTATGGGAGAGCTGTTCAATCCAGTGTAACTTTGATGTCG 411  
Db 572 CTTACCTTACCGTCCAAAGTTATGGGAGAGCTGTTCAATCCAGTGTAACTTTGATGTCG 631  
QY 412 CTGAGATGACCTTGTGAAGTACTGTCTACCTCCACATGACCTGACCGCCGCGGATA 471  
Db 632 CTGAGATGACCTTGTGAAGTACTGTCTACCTCCACATGACCTGACCGCCGCGGATA 691  
QY 472 TTTCTCTGGGAGCTCGGTCTCTCTGTCAGCCATTCAGCTATTTATTTTTCGAGGCCCA 531  
Db 692 TTTCTCTGGGAGCTCGGTCTCTCTGTCAGCCATTCAGCTATTTATTTTTCGAGGCCCA 751  
QY 532 GCGACCTTCAAAGTGCAGTGAAGATCTGCTCTGACCCCAACAGCAATGGGACTTTGA 591  
Db 752 GCGACCTTCAAAGTGCAGTGAAGATCTGCTCTGACCCCAACAGCAATGGGACTTTGA 811  
QY 592 CTTTCGCTGGTACTCGAGAGCTGAGCCCGCAAGTCTGCAACTGTAAATCTCACTG 651  
Db 812 CTTTCGCTGGTACTCGAGAGCTGAGCCCGCAAGTCTGCAACTGTAAATCTCACTG 871  
QY 652 TGATTCGGTGTCCC 665  
Db 872 TGATTCGGTGTCCC 885

## RESULT 2

LOCUS BX358190 1201 bp mRNA linear EST 05-MAY-2003  
DEFINITION BX358190 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CS0DI035YC01 5-PRIME, mRNA sequence.  
ACCESSION BX358190  
VERSION BX358190.1 GI:30372233  
KEYWORDS EST.

## SOURCE

ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)

## COMMENT

Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 10299.f  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0DI035AB01QPI.

## FEATURES

source

1. .1201  
/organism="Homo sapiens"  
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/clone="CS0DI035YC01"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo (dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 42.4%; Score 498; DB 13; Length 1201;  
Best Local Similarity 100.0%; Pred. No. 1.5e-237;  
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 678 GGTGGTATTAATATTCAGGTGTATTAATCAAGTTTACCGAGTTAGGTTTTCATGCGCT 737  
Db 64 GGTGGTATTAATATTCAGGTGTATTAATCAAGTTTACCGAGTTAGGTTTTCATGCGCT 123  
QY 738 ACTTGGGGCAAGTGTGACTTGGACTAGCAGGACCACATCTTCTGACGGCGACGTACT 797  
Db 124 ACTTGGGGCAAGTGTGACTTGGACTAGCAGGACCACATCTTCTGACGGCGACGTACT 183  
QY 798 CTTACAATACGCTGCTGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 857  
Db 184 CTTACAATACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243  
QY 858 TGTGTTTCTGCTGTGAG 917  
Db 244 TGTGTTTCTGCTGTGAG 303  
QY 918 AAAG 977  
Db 304 AAAG 363  
QY 978 TCAGATGAACAAAGAACACACAGACCGCTTCTCCCTCCCAAAATCTGTGATCCAGT 1037  
Db 364 TCAGATGAACAAAGAACACACAGACCGCTTCTCCCTCCCAAAATCTGTGATCCAGT 423  
QY 1038 GATCCTGAG 1097  
Db 424 GATCCTGAG 483  
QY 1098 CCCAGGCCAGCAAGTCATCCACAGGCTTCTTTTAATCTGGCCAGTCTGAGAGAGGTCAGT 1157  
Db 484 CCCAGGCCAGCAAGTCATCCACAGGCTTCTTTTAATCTGGCCAGTCTGAGAGAGGTCAGT 543  
QY 1158 AATACAACTGTAGTATAG 1175  
Db 544 AATACAACTGTAGTATAG 561

## RESULT 3



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BX370118      917 bp      mRNA      linear      EST 08-MAY-2003
LOCUS      BX370118 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION      clone CS0D1076YN22 5-PRIME, mRNA sequence.
ACCESSION      BX370118
VERSION      BX370118.1 GI:30447910
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 917)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2250.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAG037ZE05_CS03493_2&cluster=2250.r.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAG037ZE05_CS03493_2.
Location/Qualifiers
1. .917
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source
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Best Local Similarity 99.8%; Pred. No. 4.6e-215;
Matches 503; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      672      ACTGGAGGTGGTATTATATCCAGGTGTTATATCAAGTTACCGAGTTAGGTTTTC 731
Db      31      ACTGGAGGTGGTATTATATCCAGGTGTTATATCAAGTTACCGAGTTAGGTTTTC 90

QY      732      TTGCCTACTTGGGGCAAAAGTTGGACTTGGACTAGCAGGCACCATGCTTCTGACGCCGACG 791
Db      91      TTGCCTACTTGGGGCAAAAGTTGGACTTGGACTAGCAGGCACCATGCTTCTGACGCCGACG 150

QY      792      TGTACTCTTACATACGCTGCTGCTGCTGCGCGCGTGTGTTGTTGGTGCAACTGCTGC 851
Db      151      TGTACTCTTACATACGCTGCTGCTGCTGCGCGCGTGTGTTGTTGGTGCAACTGCTGC 210

QY      852      TGCCTGTGTTGTTTTCGCTGTAGACAAAAGAGGATTCGTATTCATTTCAAAAGAAA 911
Db      211      TGCCTGTGTTGTTTTCGCTGTAGACAAAAGAGGATTCGTATTCATTTCAAAAGAAA 270

QY      912      TCTGAAAAGAGAAGACAAACAAAGAACTTGACACAGAAAGTGAAATGAAACTCCGGC 971
Db      271      TCTGAAAAGAGAAGACAAACAAAGAACTTGACACAGAAAGTGAAATGAAACTCCGGC 330

QY      972      TACAATTCAGATGAAACAAAGACACACAGACACGCTTCTCTCCCTCCCAATCCTGTGAA 1031
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QY      1032      TCCAGTGATCCTGAAACAAAGAAACAGTACTGTGGCCCTCTCACCAGCGGGGTGATCAA 1091
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QY      1092      CGTCCACCCAGGCCAGCAAGTCAATCACAGGGCTCTTTTAATCTGGCCAGTCTCTGAGAAG 1151
Db      451      CGTCCACCCAGGCCAGCAAGTCAATCACAGGGCTCTTTTAATCTGGCCAGTCTCTGAGAAG 510

QY      1152      GTCAGTAATAACAACACTCTAGTATAG 1175
Db      511      GTCAGTAATAACAACACTCTAGTATAG 534

RESULT 4
BX403420
LOCUS      BX403420 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION      clone CS0D1085YA24 5-PRIME, mRNA sequence.
ACCESSION      BX403420
VERSION      BX403420.1 GI:30607302
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 941)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
10299.f, and it belongs to a clone representative of this cluster.
For more information about this cluster and the virtual cDNA, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS5AA017ZE02RM1&cluster=10299.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS5AA017ZE02RM1.
Location/Qualifiers
1. .941
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1085YA24"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source
Query Match      37.7%; Score 443; DB 13; Length 941;
Best Local Similarity 100.0%; Pred. No. 4.6e-210;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      52      GTTCTGGGCTCGTGAATGAAGTCATAGAGGGCCCCAGATGCAACAGTCTCAAGGGCT 111
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QY      112      CCCAGGCTCGCTTCAACTGCACCGCTCCAGGGCTGGAGGCTCATCATGTGGCTCTCA 171
Db      346      CCCAGGCTCGCTTCAACTGCACCGCTCCAGGGCTGGAGGCTCATCATGTGGCTCTCA 405

QY      172      GTGACATGTTGTTGTTAAGCGTCAGGCCCATGAGCCCATCATCAATGACCGCTTCA 231
Db      406      GTGACATGTTGTTGTTAAGCGTCAGGCCCATGAGGCCCATCATCAATGACCGCTTCA 465

QY      232      CCTCTCAGAGGTACGACAGGGGGGAACTTCACTCGGAGATGATCATCAATGTGG 291
Db      466      CCTCTCAGAGGTACGACAGGGGGGAACTTCACTCGGAGATGATCATCAATGTGG 525

QY      292      AGCCCAAGTATTTCGGGGAAACATCAGATGACGCTCCAGAACAGTGCCTGATGATCTG 351
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```

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526 AGCCAGTGAATTCGGGGAACATCAGATGAGCCTCCAGAACAGTGCCTGCATGATCTG 585
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352 CTTACTTACCGTCCAAAGTTATGGAGAGCTGTTCAATCCAGTGTATTAATCTTGATGCG 411
|||||
586 CTTACTTACCGTCCAAAGTTATGGAGAGCTGTTCAATCCAGTGTATTAATCTTGATGCG 645
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412 CTGAGAAATGAACCTTGTAAGTTACTTGTTACCTCTCACACTGGACCGGCTCCCGGATA 471
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646 CTGAGAAATGAACCTTGTAAGTTACTTGTTACCTCTCACACTGGACCGGCTCCCGGATA 705
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472 TTTCCTGGGAGCTCGGCTCTCCTG 494
|||||
706 TTTCCTGGGAGCTCGGCTCTCCTG 728

RESULT 5
BX370209 970 bp mRNA linear EST 08-MAY-2003
LOCUS BX370209 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1085YA24 5-PRIME, mRNA sequence.
ACCESSION BX370209
VERSION BX370209.1 GI:30451880
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 970)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10299.f, and
it belongs to a clone representative of this cluster. For more
information about this cluster and the virtual cDNA, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAG039ZE05_CS03685_1&cluster=10299.f.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/InvitrogenCorporation1600
Faraday Avenue Genoscope sequence ID : CS0BAG039ZE05_CS03685_1.

FEATURES
Location/Qualifiers
1..970
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1085YA24"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 27.9%; Score 328; DB 13; Length 970;
Best Local Similarity 100.0%; Pred. No. 1.7e-152;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 673 CTGGAGGTGGTATTAATATTCAGAGTGTATTATCAAGTTTACCGAGTTTAGGTTTTCAT 732
DB 32 CTGGAGGTGGTATTAATATTCAGAGTGTATTATCAAGTTTACCGAGTTTAGGTTTTCAT 91
QY 733 TGCCTACTTGGGCAAGTTGGACTTGGACTAGCAGGCACCATGCTTCTGACGCCGACGT 792
DB 92 TGCCTACTTGGGCAAGTTGGACTTGGACTAGCAGGCACCATGCTTCTGACGCCGACGT 151
QY 793 GTACTCTTACATACCGTGTCTGTGCGCGCGTGTGTTGTTGGCTGCAACTGTGCT 852
|||||

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DB 152 GTACTCTTACATACGCTGCTGCTGCGCGCTGTTGTTGTGCTGCAACTGCTGCT 211
QY 853 GCCGTTGTTGTTCTGCTGTAGAGAAAGAGAGGATTTTCGTTATCAATTTCAAAAGAAAT 912
DB 212 GCCGTTGTTGTTCTGCTGTAGAGAAAGAGAGGATTTTCGTTATCAATTTCAAAAGAAAT 271
QY 913 CTGAAAAGAGAGAGCAAAACAAAGAACTGAGACAGAAAGTGGAATGAAAATCTCCGGT 972
DB 272 CTGAAAAGAGAGAGCAAAACAAAGAACTGAGACAGAAAGTGGAATGAAAATCTCCGGT 331
QY 973 ACAATTCAGATCAACAAAAGACCACAGA 1000
DB 332 ACAATTCAGATCAACAAAAGACCACAGA 359

RESULT 6
BG740428 725 bp mRNA linear EST 15-MAY-2001
LOCUS BG740428 Homo sapiens cDNA clone IMAGE:4778789 5',
DEFINITION mRNA sequence.
ACCESSION BG740428
VERSION BG740428.1 GI:14051081
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 725)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10635 row: b column: 06
High quality sequence stop: 725.

FEATURES
Location/Qualifiers
1..725
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4778789"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Skn3"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match 22.7%; Score 267; DB 12; Length 725;
Best Local Similarity 100.0%; Pred. No. 5.3e-122;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 908 GAAATCTGAAAAGAGAGACAAAACAAAGAACTGAGACAGAAAGTGGAATGAAAATCTC 967
DB 379 GAAATCTGAAAAGAGAGACAAAACAAAGAACTGAGACAGAAAGTGGAATGAAAATCTC 438
QY 968 CGGCTACAAATTCAGATGAAACAAAGAACACACACACCGCTTCTCTCCCTCCCAATCTCG 1027
DB 439 CGGCTACAAATTCAGATGAAACAAAGAACACACACACCGCTTCTCTCCCTCCCAATCTCG 498
QY 1028 TGAATCCAGTGTCTTGAAACAAAGAACACAGTAGCTGTGGCCCTCTCTCACAGCGGCTGA 1087
DB 499 TGAATCCAGTGTCTTGAAACAAAGAACACAGTAGCTGTGGCCCTCTCTCACAGCGGCTGA 558
QY 1088 TCAAGTCCACCCAGCCAGCAAGTATCCACAGGCTTCTTTAAATCTGCCAGTCTCTGA 1147

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|||||
559 TCAAGCTCCACCCAGGCGCAGGATCATCCAGGCTTCTTTAATCTGCCAGTCTGA 618
|||||
1148 GAAGTCTAGTATACAACTGTAGTATA 1174
|||||
619 GAAGTCTAGTATACAACTGTAGTATA 645
|||||

RESULT 7
BX370210
LOCUS
DEFINITION
BX370210 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1085YA24 5-PRIME, mRNA sequence.
ACCESSION
BX370210
VERSION
BX370210.1 GI:30451881
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1148)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10299.f, and
it belongs to a clone representative of this cluster. For more
information about this cluster and the virtual cDNA, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAG039ZE05_CS03685_2&cluster=10299.f.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0BAG039ZE05_CS03685_2.
FEATURES
Location/Qualifiers
source
1..1148
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1085YA24"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 19.2%; Score 226; DB 13; Length 1148;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 665 CCAAGACACTGAGGTGGTATTAAATTCAGGTGATTATCAAGTTTCCAGGTTTAGG 724
DB 14 CCAAGACACTGAGGTGGTATTAAATTCAGGTGATTATCAAGTTTCCAGGTTTAGG 73

QY 725 TTTTTCATTGCCCTACTTGGGGCAAGTTGGACTTAGCAGGCCACCATGCTTCTGAC 784
DB 74 TTTTTCATTGCCCTACTTGGGGCAAGTTGGACTTAGCAGGCCACCATGCTTCTGAC 133

QY 785 GCGACGTGTACTCTTACATAGCTGCTGCTCTGCTGCCCGCGTGTGTGGCTGCAC 844
DB 134 GCGACGTGTACTCTTACATAGCTGCTGCTCTGCTGCCCGCGTGTGTGGCTGCAC 193

QY 845 CTGCTGCTGCCGTGTGTGTGTCTGCTGCTAGAGAAAAGAGGATTT 890
DB 194 CTGCTGCTGCCGTGTGTGTGTCTGCTGCTAGAGAAAAGAGGATTT 239

RESULT 8

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BG206666
LOCUS
DEFINITION
RST26117 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION
BG206666
VERSION
BG206666.1 GI:13728353
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 216)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R.,
Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozar, S.,
Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K.,
Offenbacher, J., Danzig, J. and Ducar, M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
JOURNAL
MEDLINE
21227151
PUBMED
11329013
COMMENT
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 166.
Location/Qualifiers
source
1..216
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
ORIGIN
Query Match 12.7%; Score 149; DB 12; Length 216;
Best Local Similarity 100.0%; Pred. No. 4.6e-63;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1018 CCAAAATCCTGTGAATCCAGTATCCTGAAACAAAGAACAGTAGCTGTGCCCTCTCACC 1077
DB 21 CCAAAATCCTGTGAATCCAGTATCCTGAAACAAAGAACAGTAGCTGTGCCCTCTCACC 80

QY 1078 AGCGGCTGATCAAGTCCACCCAGCCAGCAAGTCATCCAGGCTCTTTTAATCTGG 1137
DB 81 AGCGGCTGATCAAGTCCACCCAGCCAGCAAGTCATCCAGGCTCTTTTAATCTGG 140

QY 1138 CCAGTCTCAGAGGTCAGTATACT 1166
DB 141 CCAGTCTCAGAGGTCAGTATACT 169

RESULT 9
AG069679
LOCUS
DEFINITION
Pan troglodytes DNA, clone: PTB-060F12.F, genomic survey sequence.
ACCESSION
AG069679
VERSION
AG069679.1 GI:16621481
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

```

Totoki,Y., Watanabe,H. and Sakaki,Y.  
BAC end sequences of Library PTB  
Unpublished  
2 (bases 1 to 622)  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
Direct Submission  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail:chimpesgsc.riken.go.jp, URL:http://hgp.riken.go.jp/,  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.  
PRIMERS

Sequencing: -21M13  
LIBRARY  
Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI.  
Location/Qualifiers  
1. 622  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-060F12.F"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC Library"

FEATURES  
source

ORIGIN  
Query Match 12.4%; Score 146; DB 29; Length 622;  
Best Local Similarity 100.0%; Pred.No. 1.9e-61;  
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 479 GGAGCTCGGTCTCTCGTGCAGCCATTCAAGCTATTATTGTTCCGGAGCCCGACCT 538  
Db 77 GGAGCTCGGTCTCTCGTGCAGCCATTCAAGCTATTATTGTTCCGGAGCCCGACCT 136

QY 539 TCAAGTGCAGTGCATCTCGCTGACCCACAGAGCAATGGACTTTCACCTTGCCT 598  
Db 137 TCAAGTGCAGTGCATCTCGCTGACCCACAGAGCAATGGACTTTCACCTTGCCT 196

QY 599 GGCTACCTGGAGAGCCTGAAGGCC 624  
Db 197 GGCTACCTGGAGAGCCTGAAGGCC 222

RESULT 10  
AG107877  
LOCUS AG107877 677 bp DNA linear GSS 03-NOV-2001  
DEFINITION Pan troglodytes DNA, clone: PTB-112N07.F, genomic survey sequence.  
ACCESSION AG107877  
VERSION AG107877.1 GI:16728395  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.  
1  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
BAC end sequences of Library PTB  
Unpublished  
2 (bases 1 to 677)  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
Direct Submission  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail:chimpesgsc.riken.go.jp, URL:http://hgp.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.  
PRIMERS

Sequencing: -21M13  
LIBRARY  
Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI.  
Location/Qualifiers  
1. 677  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-112N07.F"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC Library"

FEATURES  
source

ORIGIN  
Query Match 12.4%; Score 146; DB 29; Length 677;  
Best Local Similarity 100.0%; Pred.No. 1.9e-61;  
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 479 GGAGCTCGGTCTCTCGTGCAGCCATTCAAGCTATTATTGTTCCGGAGCCCGACCT 538  
Db 77 GGAGCTCGGTCTCTCGTGCAGCCATTCAAGCTATTATTGTTCCGGAGCCCGACCT 136

QY 539 TCAAGTGCAGTGCATCTCGCTGACCCACAGAGCAATGGACTTTCACCTTGCCT 598  
Db 137 TCAAGTGCAGTGCATCTCGCTGACCCACAGAGCAATGGACTTTCACCTTGCCT 196

QY 599 GGCTACCTGGAGAGCCTGAAGGCC 624  
Db 197 GGCTACCTGGAGAGCCTGAAGGCC 222

RESULT 11  
BX358189/c  
LOCUS BX358189 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
DEFINITION clone CSOD1035YC01 3-PRIME, mRNA sequence.  
ACCESSION BX358189  
VERSION BX358189.1 GI:30370198  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 1201)  
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequenage  
BP 191 91006 EVRY cedex - France  
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 10299.f  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CSOD1035AB01NP1.  
Location/Qualifiers  
1. 1201  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSOD1035YC01"  
/tissue type="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 9.4%; Score 110; DB 13; Length 1201;  
Best Local Similarity 100.0%; Pred. No. 2.3e-43;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1066 GCCCTCCTCACAGCGGCTGATCAACGTCCACCAGCCAGCAAGTCATCCACAGGCTT 1125  
Db 811 GCCCTCCTCACAGCGGCTGATCAACGTCCACCAGCCAGCAAGTCATCCACAGGCTT 752  
QY 1126 CTTTAACTCGCCAGTCTGAGAGGTCAGTAATACAACTGTAGTATAG 1175  
Db 751 CTTTAACTCGCCAGTCTGAGAGGTCAGTAATACAACTGTAGTATAG 702

## RESULT 12

N47851 185 bp mRNA linear EST 14-FEB-1996  
LOCUS YW95h05.r1 Soares\_placenta\_8to9weeks\_2NBHP8to9W Homo sapiens cDNA  
DEFINITION clone IMAGE:260025 5', mRNA sequence.

## ACCESSION

N47851

## VERSION

N47851.1 GI:1189017

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 185)  
Hillier, L., Clark, N., Dubucque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and  
Wilson, R.

## TITLE

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: T7

High quality sequence stop: 150.

Location/Qualifiers

1..185

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3889731"

/db\_xref="taxon:9606"

/clone="IMAGE:260025"

/dev\_stage="two placentae: one from 8 weeks and another

from 9 weeks post conception"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares\_placenta\_8to9weeks\_2NBHP8to9W"

/notes="Organ: placenta; Vector: pT7T3D (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGGCGGATTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library constructed by Bento Soares and

M.Fatima Bonaldo."

## ORIGIN

Query Match 8.5%; Score 100; DB 14; Length 185;  
Best Local Similarity 100.0%; Pred. No. 1.5e-38;  
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1076 CCAGCGGGCTGATCAACGTCCACCAGCCAGCAAGTCATCCACAGGCTTCTTTAACT 1135  
Db 73 CCAGCGGGCTGATCAACGTCCACCAGCCAGCAAGTCATCCACAGGCTTCTTTAACT 132

QY 1136 GCCAGTCTCTGAGAGGTCAGTAATACAACTGTAGTATAG 1175  
Db 133 GCCAGTCTCTGAGAGGTCAGTAATACAACTGTAGTATAG 172

## RESULT 13

N93995

## LOCUS

za66f09.r1 Soares\_fetal\_lung NBHL19W Homo sapiens cDNA clone

IMAGE:297545 5', mRNA sequence.

## ACCESSION

N93995

## VERSION

N93995.1 GI:1266304

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 234)

Hillier, L., Clark, N., Dubucque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and

Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: mob.REGA+ET

High quality sequence stop: 159.

Location/Qualifiers

1..234

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:1242467"

/db\_xref="taxon:9606"

/clone="IMAGE:297545"

/dev\_stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares\_fetal\_lung NBHL19W"

/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer

[5'-TGTTACCAATCTGAAGTGGAGCGGCGGCAATTTTTTTTTTTT-3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo. This library was constructed

from the same fetus as the fetal heart library, Soares

fetal heart NBHL19W."

## ORIGIN

Query Match 8.5%; Score 100; DB 14; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.6e-38;  
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1076 CCAGCGGGCTGATCAACGTCCACCAGCCAGCAAGTCATCCACAGGCTTCTTTAACT 1135  
Db 113 CCAGCGGGCTGATCAACGTCCACCAGCCAGCAAGTCATCCACAGGCTTCTTTAACT 172

QY 1136 GGCCAGTCTCTGAGAGGTCAGTAATACAACTGTAGTATAG 1175

173 GCCCAGTCTCGAAGGTGACGTGATATCAACTGTAGTATAG 212

Db

RESULT 14  
AQ403719/c

LOCUS  
DEFINITION  
HS\_5049\_A1\_C11\_T7A RPCI-11 Human Male BAC Library Homo sapiens  
genomic clone Plate=625 Col=21 Row=E, genomic survey sequence.

ACCESSION  
AQ403719

VERSION  
KEYWORDS  
GSS.

SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens

REFERENCE  
AUTHORS  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,  
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D., and  
Hood, L.B.

TITLE  
Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome

JOURNAL  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

MEDLINE  
99380589

PUBMED  
10449764

COMMENT  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact Pieter de Jong  
[pieter@dejong.med.buffalo.edu]. Clones may be purchased from  
BACPAC Resources ([http://bacpac.med.buffalo.edu/ordering\\_bac.htm](http://bacpac.med.buffalo.edu/ordering_bac.htm))  
or from Research Genetics (<http://info@resgen.com>). BAC end Web Server:  
<http://www.htsc.washington.edu>  
Plate: 625 row: E column: 21  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 525.

FEATURES  
source  
Location/Qualifiers  
1..525  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="Plate=625 Col=21 Row=E"  
/sex="male"  
/clone\_lib="RPCI-11 Human Male BAC Library"  
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRI Methylase. Size selected DNA was cloned into the  
pBACe3.6 vector at EcoRI sites"

ORIGIN  
Query Match 6.5%; Score 76; DB 28; Length 525;  
Best Local Similarity 100.0%; Pred. No. 1.9e-26;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1100 CAGGCCAGCAGTATCCACAGGCTCTTTTAATCTGCCAGTCTCGAGAGGTCAGTAA 1159  
|||||  
Db 347 CAGGCCAGCAGTATCCACAGGCTCTTTTAATCTGCCAGTCTCGAGAGGTCAGTAA 288  
|||||

QY 1160 TACAACTGTAGTATAG 1175  
|||||  
Db 287 TACAACTGTAGTATAG 272  
|||||

RESULT 15  
CK230652

LOCUS  
DEFINITION  
ILLUMIGEN\_MQ0\_1006 Katze\_WMP12 Macaca mulatta cDNA 5' similar to

human LOC150084 (Hs.422120), mRNA sequence.

ACCESSION  
CK230652

VERSION  
KEYWORDS  
EST.

SOURCE  
Macaca mulatta (rhesus monkey)

ORGANISM  
Macaca mulatta

REFERENCE  
AUTHORS  
Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magnus, C.L.  
Large-scale Rhesus Macaque cDNA Sequencing  
Unpublished (2003)  
Contact: C. Magnus  
Illumigen Biosciences Inc.  
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
Tel: 2063780400  
Fax: 2063780408  
Email: cmagnus@illumigen.com  
Sequenced on 2003.10.16. 695 020 bases. Assemblies in contig w/ 1  
member(s). Contig contains 1 (0%) lib members.

TITLE  
PCR Primers

JOURNAL  
COMMENT  
FORWARD: CCTCACTAAAGGGAACAAAA  
BACKWARD: CACTATAGGGCGAATTGGGTA  
Insert Length: 976 Std Error: 0.00  
Plate: CL000009 row: C column: 07  
Seq primer: CCTCACTAAAGGGAACAAAA  
POLYA=No.

FEATURES  
Location/Qualifiers  
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/organism="Macaca mulatta"  
/mol\_type="mRNA"  
/strain="Indian"  
/db\_xref="taxon:9544"  
/sex="male"  
/dev\_stage="newborn infant"  
/lab\_host="E. coli SOLR"  
/clone\_lib="Katze\_WMP12"  
/note="Organ: placenta; Vector: Uni-ZAP XR; Site 1: EcoR  
I; Site 2: Xho I; Created from Stratagene ZAP-CDNA  
Synthesis kit (catalog #200400) and ZAP-CDNA Gigapack II  
Gold Cloning Kit (Catalog #200450)"

ORIGIN  
Query Match 5.4%; Score 63; DB 14; Length 976;  
Best Local Similarity 100.0%; Pred. No. 7.2e-20;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 AGCCCACTGATTCGGGGAACATCAGATGCAGCTCCAGACAGTGCCTCGATGATCTG 351  
|||||  
Db 581 AGCCCACTGATTCGGGGAACATCAGATGCAGCTCCAGACAGTGCCTCGATGATCTG 640  
|||||

QY 352 CTT 354  
|||  
Db 641 CTT 643  
|||

Search completed: September 15, 2004, 06:43:43  
Job time : 3452.95 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 22:59:39 ; Search time 3426.42 Seconds  
(without alignments)  
10179.449 Million cell updates/sec

Title: US-09-729-264-3

Perfect score: 1168

Sequence: 1 agtgatcatggggcaggag.....gtaatacaactgtagtatag 1168

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55024014

Minimum DB seq length: 16

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estnu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_estl:\*
- 10: gb\_est2:\*
- 11: gb\_htc:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_inv:\*
- 19: em\_gss\_pln:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_man:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_rod:\*
- 26: em\_gss\_phg:\*
- 27: em\_gss\_vrl:\*
- 28: gb\_gssl:\*
- 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	517	44.3	1201	13	EX399881
2	498	42.6	1201	13	EX358190
3	453	38.8	917	13	EX370118
4	361	30.9	941	13	EX403420

	5	328	28.1	970	13	EX370209	1201 bp	mrna	linear	EST 13-MAY-2003
6	267	22.9	725	12	BG740428	BX370209	1201 bp	mrna	linear	EST 13-MAY-2003
7	226	19.3	1148	13	BX370210	BX370210	1201 bp	mrna	linear	EST 13-MAY-2003
8	149	12.8	216	12	BG206666	BG206666	1201 bp	mrna	linear	EST 13-MAY-2003
9	146	12.5	622	29	AG069679	AG069679	1201 bp	mrna	linear	EST 13-MAY-2003
10	146	12.5	677	29	AG107877	AG107877	1201 bp	mrna	linear	EST 13-MAY-2003
c	11	110	9.4	1201	13	BX358189	1201 bp	mrna	linear	EST 13-MAY-2003
12	100	8.6	185	14	N47851	N47851	1201 bp	mrna	linear	EST 13-MAY-2003
13	100	8.6	234	14	N91995	N91995	1201 bp	mrna	linear	EST 13-MAY-2003
c	14	76	6.5	225	28	AQ403719	1201 bp	mrna	linear	EST 13-MAY-2003
15	63	5.4	976	14	CK230652	CK230652	1201 bp	mrna	linear	EST 13-MAY-2003
16	45	3.9	983	14	CK230612	CK230612	1201 bp	mrna	linear	EST 13-MAY-2003
17	34	2.9	527	10	BE032610	BE032610	1201 bp	mrna	linear	EST 13-MAY-2003
c	18	33	2.8	685	29	AG142221	1201 bp	mrna	linear	EST 13-MAY-2003
c	19	27	2.3	565	14	CD344913	1201 bp	mrna	linear	EST 13-MAY-2003
20	25	2.1	635	28	AQ541776	AQ541776	1201 bp	mrna	linear	EST 13-MAY-2003
c	21	24	2.1	68	29	AB082057	1201 bp	mrna	linear	EST 13-MAY-2003
c	22	24	2.1	680	9	AA941851	1201 bp	mrna	linear	EST 13-MAY-2003
c	23	23	2.0	219	13	BQ862485	1201 bp	mrna	linear	EST 13-MAY-2003
c	24	23	2.0	291	28	AZ411779	1201 bp	mrna	linear	EST 13-MAY-2003
c	25	23	2.0	316	13	BQ864023	1201 bp	mrna	linear	EST 13-MAY-2003
c	26	23	2.0	631	10	B8663870	1201 bp	mrna	linear	EST 13-MAY-2003
27	23	2.0	664	28	BH020641	BH020641	1201 bp	mrna	linear	EST 13-MAY-2003
28	23	2.0	773	14	CB648901	CB648901	1201 bp	mrna	linear	EST 13-MAY-2003
29	23	2.0	784	12	BG863468	BG863468	1201 bp	mrna	linear	EST 13-MAY-2003
30	23	2.0	794	10	BF784177	BF784177	1201 bp	mrna	linear	EST 13-MAY-2003
31	23	2.0	1510	11	AK086973	AK086973	1201 bp	mrna	linear	EST 13-MAY-2003
32	22	1.9	167	29	CG475380	CG475380	1201 bp	mrna	linear	EST 13-MAY-2003
33	22	1.9	171	29	CG480695	CG480695	1201 bp	mrna	linear	EST 13-MAY-2003
34	22	1.9	188	13	BQ134412	BQ134412	1201 bp	mrna	linear	EST 13-MAY-2003
35	22	1.9	196	29	CG480560	CG480560	1201 bp	mrna	linear	EST 13-MAY-2003
36	22	1.9	219	29	CG479279	CG479279	1201 bp	mrna	linear	EST 13-MAY-2003
37	22	1.9	223	29	CG615044	CG615044	1201 bp	mrna	linear	EST 13-MAY-2003
38	22	1.9	232	29	CG481750	CG481750	1201 bp	mrna	linear	EST 13-MAY-2003
39	22	1.9	234	29	CG481764	CG481764	1201 bp	mrna	linear	EST 13-MAY-2003
40	22	1.9	238	29	CG566401	CG566401	1201 bp	mrna	linear	EST 13-MAY-2003
c	41	22	1.9	287	10	BB343618	1201 bp	mrna	linear	EST 13-MAY-2003
c	42	22	1.9	328	29	CG476832	1201 bp	mrna	linear	EST 13-MAY-2003
c	43	22	1.9	340	14	Z46691	1201 bp	mrna	linear	EST 13-MAY-2003
c	44	22	1.9	376	28	CC179595	1201 bp	mrna	linear	EST 13-MAY-2003
c	45	22	1.9	424	9	AV409989	1201 bp	mrna	linear	EST 13-MAY-2003

#### ALIGNMENTS

RESULT 1  
BX399881  
LOCUS  
DEFINITION  
BX399881 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
clone CS0D1085YA24 5-PRIME, mRNA sequence.  
ACCESSION  
BX399881  
VERSION  
BX399881.1  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
JOURNAL  
COMMENT  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 10299.f, and  
it belongs to a clone representative of this cluster. For more  
information about this cluster and the virtual cDNA, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0D1085BA12QPI&cluster=10299.f. Contact :  
Feng Liang Email : fliang@lifetech.com URL :

BX399881 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
clone CS0D1085YA24 5-PRIME, mRNA sequence.

BX399881.1 GI:30622019

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 10299.f, and  
it belongs to a clone representative of this cluster. For more

information about this cluster and the virtual cDNA, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0D1085BA12QPI&cluster=10299.f. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Paradise Avenue Genoscope sequence ID : CS0DI085BA12QP1.

FEATURES

source  
1. .1201  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DI085YA24"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 44.3%; Score 517; DB 13; Length 1201;  
Best Local Similarity 99.8%; Pred. No. 2e-245;  
Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 91 AGTCTCTGAAGGCTCCAGGCTCGCTTCAACTGCACCGCTCCAGGGCTGGAAGCTCAT 150  
Db 318 AGTCTCTGAAGGCTCCAGGCTCGCTTCAACTGCACCGCTCCAGGGCTGGAAGCTCAT 377  
QY 151 CATGTGGGCTCTCAAGTACATGATGCTGTCTAAGCGTTCAGGCCCATGAGGCCCATCATCAC 210  
Db 378 CATGTGGGCTCTCAAGTACATGATGCTGTCTAAGCGTTCAGGCCCATGAGGCCCATCATCAC 437  
QY 211 CAATGACCGCTTCACTCTCAGAGGTACACAGGCGGGAACCTTCACTCGAGATGAT 270  
Db 438 CAATGACCGCTTCACTCTCAGAGGTACACAGGCGGGAACCTTCACTCGAGATGAT 497  
QY 271 CATCACAAATGTGGGCCAGTGTATTCGGGGAACATCAGATGAGCTCCAGAACAGTCG 330  
Db 498 CATCACAAATGTGGGCCAGTGTATTCGGGGAACATCAGATGAGCTCCAGAACAGTCG 557  
QY 331 CTGATGATGATCTGCTTACCTTACCGTCCAAAGTATGAGGAGCTGTTCATTTCCCAAGTGT 390  
Db 558 CTGATGATGATCTGCTTACCTTACCGTCCAAAGTATGAGGAGCTGTTCATTTCCCAAGTGT 617  
QY 391 TAATCTTGTAGTGTGAGAAATGAACCTTGTGAAGTATCTGTACCTCTACCTCTCAGTGGAC 450  
Db 618 TAATCTTGTAGTGTGAGAAATGAACCTTGTGAAGTATCTGTACCTCTACCTCTCAGTGGAC 677  
QY 451 CTGGCTCCCGGATATTTCTGGAGCTCGCTCTCTCTGGTTCAGCATTCAAGCTATTATTT 510  
Db 678 CCGGCTCCCGGATATTTCTGGAGCTCGCTCTCTCTGGTTCAGCATTCAAGCTATTATTT 737  
QY 511 TGTTCGGGAGCCAGGACCTTCAAGTGCAGTGAGCATCTCTGGCTTCGACCCCAAGAG 570  
Db 738 TGTTCGGGAGCCAGGACCTTCAAGTGCAGTGAGCATCTCTGGCTTCGACCCCAAGAG 797  
QY 571 CAATGGGACTTTCAGTTCGTGGTACCTTGGAGAGCTTGAAGCCCGGAGCTGCTGCAAC 630  
Db 798 CAATGGGACTTTCAGTTCGTGGTACCTTGGAGAGCTTGAAGCCCGGAGCTGCTGCAAC 857  
QY 631 TGTAAATCTCACTGTGATTCGGTGTCCC 658  
Db 858 TGTAAATCTCACTGTGATTCGGTGTCCC 885

RESULT 2

LOCUS BX358190  
DEFINITION BX358190 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CS0DI035YC01 5-PRIME, mRNA sequence.  
ACCESSION BX358190  
VERSION BX358190.1 GI:30372233  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1201)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)

COMMENT

Genoscope - Centre National de Sequencage  
Bp 191 91006 EVRY cedex - France  
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 10299.f  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Paradise Avenue Genoscope sequence ID : CS0DI035BA01QP1.

FEATURES

source

1. .1201  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DI035YC01"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 42.6%; Score 498; DB 13; Length 1201;  
Best Local Similarity 100.0%; Pred. No. 5.6e-236;  
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 671 GGTGGTATTATTAATTCAGGCTGATTATCAAGTTTACCGAGTTTAGGTTTTTCATTGCGCT 730  
Db 64 GGTGGTATTATTAATTCAGGCTGATTATCAAGTTTACCGAGTTTAGGTTTTTCATTGCGCT 123  
QY 731 ACTTGGGGCAAAAGTTGGACTTGGACTAGCAGGCACCATGCTTCTGACGCCGACGTGACT 790  
Db 124 ACTTGGGGCAAAAGTTGGACTTGGACTAGCAGGCACCATGCTTCTGACGCCGACGTGACT 183  
QY 791 CTTACAATACGCTGCTGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 850  
Db 184 CTTACAATACGCTGCTGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243  
QY 851 TCTTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 910  
Db 244 TCTTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303  
QY 911 AAAGAAGACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 970  
Db 304 AAAGAAGACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 363  
QY 971 TCAGATGAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1030  
Db 364 TCAGATGAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 423  
QY 1031 GATCCTGTAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1090  
Db 424 GATCCTGTAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 483  
QY 1091 CCCAGGCGAGCAAGTCATCCACAGGCTTCTTTTAAATCTGGCCAGTCTTGGAGAGGTGAGT 1150  
Db 484 CCCAGGCGAGCAAGTCATCCACAGGCTTCTTTTAAATCTGGCCAGTCTTGGAGAGGTGAGT 543  
QY 1151 AATACAACTGTAGTATAG 1168  
Db 544 AATACAACTGTAGTATAG 561

RESULT 3

LOCUS BX370118  
DEFINITION BX370118 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CS0DI076YN22 5-PRIME, mRNA sequence.  
EST. 917 bp  
linear  
BX370118 EST 08-MAY-2003



```

ACCESSION BX370118
VERSION BX370118.1 GI:30447910
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2250.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAG0372E05_CS03493_2&cluster=2250.r.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAG0372E05_CS03493_2.
Location/Qualifiers
1. .917
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1076YN22"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
FEATURES
source
Query Match 38.8%; Score 453; DB 13; Length 917;
Best Local Similarity 99.8%; Pred. No. 1.3e-213;
Matches 503; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 665 ACTGGAGTGGTATTATATTCAGGTGTTATATCAAGTTACGAGTTAGGTTTTCA 724
Db 31 ACTGGAGTGGTATTATATTCAGGTGTTATATCAAGTTACGAGTTAGGTTTTCA 90
QY 725 TTGCCTACTTGGGCAAGTTGACTTGGACTAGCAGSCCACTGCTTCTGACGCCGACG 784
Db 91 TTGCCTACTTGGGCAAGTTGACTTGGACTAGCAGSCCACTGCTTCTGACGCCGACG 150
QY 785 TGTACTCTTACAATACGCTGCTGCTGCGCGCGTGTGTTGTTGCTGCAACTGCTGC 844
Db 151 TGTACTCTTACAATACGCTGCTGCTGCGCGCGTGTGTTGTTGCTGCAACTGCTGC 210
QY 845 TCGCGTGTGTTTCTGCTAGAGAAAAGAGGATTCGTATCAATTTCAAAAGAAA 904
Db 211 TCGCGTGTGTTTCTGCTAGAGAAAAGAGGATTCGTATCAATTTCAAAAGAAA 270
QY 905 TCTGAAAAGAGAGAACAAAGAACTGACACAGAAAGTGAATGAAACTCCGCG 964
Db 271 TCTGAAAAGAGAGAACAAAGAACTGACACAGAAAGTGAATGAAACTCCGCG 330
QY 965 TACAATTCAGATGAACAAAGACCAAGACACACGCTTCTCTCCCTCCCAATCCTGTGA 1024
Db 331 TACAATTCAGATGAACAAAGACCAAGACACACGCTTCTCTCCCTCCCAATCCTGTGA 390
QY 1025 TCCAGTGATCTGAACAAAGAAACAGTAGCTGTGGCCCTCTCCACGAGCGGCTGATCAA 1084
Db 391 TCCAGTGATCTGAACAAAGAAACAGTAGCTGTGGCCCTCTCCACGAGCGGCTGATCAA 450
QY 1085 CGTCCACCCAGGCCAGCAAGTCAATCCACAGGCTTCTTTAATCTGGCCAGTCTGAGAAG 1144
Db 451 CGTCCACCCAGGCCAGCAAGTCAATCCACAGGCTTCTTTAATCTGGCCAGTCTGAGAAG 510

ORIGIN
source
Query Match 30.9%; Score 361; DB 13; Length 941;
Best Local Similarity 100.0%; Pred. No. 7.1e-168;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 AGTCCTGAAGGGCTCCAGGCTCCACTCGCTCCAGCGCTCCAGGGCTGGAAGCTCAT 150
Db 332 AGTCCTGAAGGGCTCCAGGCTCCACTCGCTCCAGCGCTCCAGGGCTGGAAGCTCAT 391
QY 151 CATGTGGCTCTCAGTGACATGTGTGTGTTAAGCGTCAGGCCCATGAGGCCCATCATC 210
Db 392 CATGTGGCTCTCAGTGACATGTGTGTGTTAAGCGTCAGGCCCATGAGGCCCATCATC 451
QY 211 CAATGACCGCTTCCACTCTCAGAGGTACGACAGGGGGAACTTCACTTCGAGATGAT 270
Db 452 CAATGACCGCTTCCACTCTCAGAGGTACGACAGGGGGAACTTCACTTCGAGATGAT 511
QY 271 CATCCCAATGTGGAGCCCAAGTGAATTCGGGGAAACATCAGATGCAGCTCCAGAACAGTCG 330
Db 512 CATCCCAATGTGGAGCCCAAGTGAATTCGGGGAAACATCAGATGCAGCTCCAGAACAGTCG 571
QY 331 CCTGCAATGATCTGCTTACCTTACCGTCCAAAGTTATGGAGAGCTTCTTATCCCAAGTGT 390
Db 572 CCTGCAATGATCTGCTTACCTTACCGTCCAAAGTTATGGAGAGCTTCTTATCCCAAGTGT 631
QY 391 TAATCTTGTAGTCGTGAGAAATCAACCTTGTGAGTACTTGTCTACCTTCACATCGGAC 450

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|||||
632 TAATCTGTAGTCGTGAGTAACCTTGTGAAGTACTTGTCTACCTCAGTGGAC 691
|||||
QY 451 C 451
Db 692 C 692

RESULT 5
BX370209 970 bp mRNA linear EST 08-MAY-2003
LOCUS
DEFINITION
BX370209 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI085YA24 5-PRIME, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 970)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10299.f, and
it belongs to a clone representative of this cluster. For more
information about this cluster and the virtual cDNA, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAG039ZE05_CS03685_1&cluster=10299.f.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0BAG039ZE05_CS03685_1.
FEATURES
Location/Qualifiers
1..970
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI085YA24"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoK v
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 28.1%; Score 328; DB 13; Length 970;
Best Local Similarity 100.0%; Pred. No. 1.8e-151;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 666 CTGGAGGTGGTATTATATCCAGGTGATTATCAAGTTTACCAGTTTAGTTTTCAT 725
Db 32 CTGGAGGTGGTATTATATATCCAGGTGATTATCAAGTTTACCAGTTTAGTTTTCAT 91
QY 726 TGCCTACTTGGGGCAAGTTGGACTTGGACTAGCAGGCACCATGCTTCTGACGCCGACGT 785
Db 92 TGCCTACTTGGGGCAAGTTGGACTTGGACTAGCAGGCACCATGCTTCTGACGCCGACGT 151
QY 786 GTACTCTTAATAGCTGCTGCTGCCCGCTGCTGTTGGTGGCTGCACTGCTGCT 845
Db 152 GTACTCTTAATAGCTGCTGCTGCCCGCTGCTGTTGGTGGCTGCACTGCTGCT 211
QY 846 GCCGTGTGTTCTTCGTGTAGAGAAAAAGAGGATTTTCGATTCAATTTCAAAAGAAAT 905
Db 212 GCCGTGTGTTCTTCGTGTAGAGAAAAAGAGGATTTTCGATTCAATTTCAAAAGAAAT 271
QY 906 CTGAAAAAGAGAAGCAAAACAAAGAACTGAGACAGAAAGTGGAAATGAAAACCTCGGCT 965
|||||

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Db 272 CTGAAAAAGAGAAGCAAAACAAAGAACTGAGACAGAAAGTGGAAATGAAAACCTCGGCT 331
QY 966 ACAATTTCAGATGAACAAAAAGACCACAGA 993
Db 332 ACAATTTCAGATGAACAAAAAGACCACAGA 359
|||||

RESULT 6
BG740428 725 bp mRNA linear EST 15-MAY-2001
LOCUS
DEFINITION
602633817E1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4778789 5',
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 725)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10635 row: b column: 06
High quality sequence stop: 725.
FEATURES
Location/Qualifiers
1..725
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4778789"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NCI_CGAP_Skn3"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Query Match 22.9%; Score 267; DB 12; Length 725;
Best Local Similarity 100.0%; Pred. No. 3.7e-121;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 901 GAAATCTGAAAAAGAGAAGCAAAACAAAGAACTGAGACAGAAAGTGGAAATGAAAACCTC 960
Db 379 GAAATCTGAAAAAGAGAAGCAAAACAAAGAACTGAGACAGAAAGTGGAAATGAAAACCTC 438
QY 961 CGGCTACAATTCAGATGAACAAAAAGACCACAGACACCGCTTCTCCCTCCCAATCTGT 1020
Db 439 CGGCTACAATTCAGATGAACAAAAAGACCACAGACACCGCTTCTCCCTCCCAATCTGT 498
QY 1021 TGAATCCAGTATCTCTGAACAAAGAAACAGTAGCTGGCCCTCCTCACCAGCGGCTGA 1080
Db 499 TGAATCCAGTATCTCTGAACAAAGAAACAGTAGCTGGCCCTCCTCACCAGCGGCTGA 558
QY 1081 TCAAGTCCACCCAGGCGCAGCAAGTCAATCCACAGGCTTCTTTTAACTGGCCAGTCTTGA 1140
Db 559 TCAAGTCCACCCAGGCGCAGCAAGTCAATCCACAGGCTTCTTTTAACTGGCCAGTCTTGA 618
QY 1141 GAAAGTCAGTAATCAACTGTAGTATA 1167
Db 619 GAAAGTCAGTAATCAACTGTAGTATA 645

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RESULT 7
BX370210      1148 bp      mRNA      linear      EST 08-MAY-2003
LOCUS
DEFINITION    clone CS0DI085YA24 5-PRIME, mRNA sequence.
ACCESSION    BX370210
VERSION      BX370210.1 GI:30451881
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1148)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10299.f, and
it belongs to a clone representative of this cluster. For more
information about this cluster and the virtual cDNA, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAG039ZE05_CS03685_2&cluster=10299.f.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAG039ZE05_CS03685_2.
FEATURES
source
Location/Qualifiers
1..1148
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI085YA24"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match      19.3%; Score 226; DB 13; Length 1148;
Best Local Similarity 100.0%; Pred. No. 9.9e-101;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 658 CCAAGACACTGGAGGTGTTATATATCCAGGTGTTATCAAGTTACCGAGTTTAGG 717
Db 14 CCAAGACACTGGAGGTGTTATATATCCAGGTGTTATCAAGTTACCGAGTTTAGG 73

QY 718 TTTTTCATTGCTTGGGCAAAAGTTGGACTGGACTAGCAGCCACCATGCTTCTGAC 777
Db 74 TTTTTCATTGCTTGGGCAAAAGTTGGACTGGACTAGCAGCCACCATGCTTCTGAC 133

QY 778 GCGACGTGACTCTTCAATACAGCTGCTGCTGCGCGCTGTTGTTGTCGCTCAA 837
Db 134 GCGACGTGACTCTTCAATACAGCTGCTGCTGCGCGCTGTTGTTGTCGCTCAA 193

QY 838 CTGCTGCTGCGCTGTTGTTGTTCTGCTAGAGAAAAGAGATT 883
Db 194 CTGCTGCTGCGCTGTTGTTGTTCTGCTAGAGAAAAGAGATT 239

RESULT 8
BG206666
LOCUS
DEFINITION    BG206666 216 bp      mRNA      linear      EST 21-APR-2001
ACCESSION    BG206666
VERSION      BG206666.1 GI:13728353
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 216)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R.,
Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S.,
Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K.,
Offenbacher, J., Danzig, J., and Ducar, M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
11329013
Contact: Scott J. Cain
Athersys, Inc. Ave, Cleveland, OH 44115, USA
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 166.
Location/Qualifiers
1..216
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

Query Match      12.8%; Score 149; DB 12; Length 216;
Best Local Similarity 100.0%; Pred. No. 1.3e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1011 CCAATCTGTGAATCCAGTATCCTGAACAAAGAACAGTAGTGTGGCCTCTCACC 1070
Db 21 CCAATCTGTGAATCCAGTATCCTGAACAAAGAACAGTAGTGTGGCCTCTCACC 80

QY 1071 AGCGGCTGATACGTCACCCAGGCCAGCAGTATCCACAGGCTCTTTTATCTGG 1130
Db 81 AGCGGCTGATACGTCACCCAGGCCAGCAGTATCCACAGGCTCTTTTATCTGG 140

QY 1131 CCAATCTGTGAAGGTGAGTAAATCAACT 1159
Db 141 CCAATCTGTGAAGGTGAGTAAATCAACT 169

RESULT 9
AG069679
LOCUS
DEFINITION    Pan troglodytes DNA, clone: PTB-060F12.F, genomic survey sequence.
ACCESSION    AG069679
VERSION      AG069679.1 GI:16621481
KEYWORDS
SOURCE
ORGANISM      Pan troglodytes (chimpanzee)

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
1
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H., and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 622)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H., and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 216)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R.,
Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S.,
Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K.,
Offenbacher, J., Danzig, J., and Ducar, M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
11329013
Contact: Scott J. Cain
Athersys, Inc. Ave, Cleveland, OH 44115, USA
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 166.
Location/Qualifiers
1..216
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

Query Match      12.8%; Score 149; DB 12; Length 216;
Best Local Similarity 100.0%; Pred. No. 1.3e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1011 CCAATCTGTGAATCCAGTATCCTGAACAAAGAACAGTAGTGTGGCCTCTCACC 1070
Db 21 CCAATCTGTGAATCCAGTATCCTGAACAAAGAACAGTAGTGTGGCCTCTCACC 80

QY 1071 AGCGGCTGATACGTCACCCAGGCCAGCAGTATCCACAGGCTCTTTTATCTGG 1130
Db 81 AGCGGCTGATACGTCACCCAGGCCAGCAGTATCCACAGGCTCTTTTATCTGG 140

QY 1131 CCAATCTGTGAAGGTGAGTAAATCAACT 1159
Db 141 CCAATCTGTGAAGGTGAGTAAATCAACT 169

RESULT 9
AG069679
LOCUS
DEFINITION    Pan troglodytes DNA, clone: PTB-060F12.F, genomic survey sequence.
ACCESSION    AG069679
VERSION      AG069679.1 GI:16621481
KEYWORDS
SOURCE
ORGANISM      Pan troglodytes (chimpanzee)

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
1
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H., and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 622)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H., and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical

```

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: chimboes@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.

## PRIMERS

Sequencing: -21M13

## LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI

Location/Qualifiers

1. .622

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

/clone="PTB-060F12.F"

/sex="male"

/cell\_type="lymphoblast"

/clone\_lib="PTB Chimpanzee Male BAC Library"

## ORIGIN

Query Match

Best Local Similarity 12.5%; Score 146; DB 29; Length 622;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 472 GGAGCTCGGTCTCTGTCAGCCATTCAAGCTATTATTGTTCCGGAGCCGACCT 531

Db 77 GGAGCTCGGTCTCTGTCAGCCATTCAAGCTATTATTGTTCCGGAGCCGACCT 136

QY 532 TCAAGTGCAGTCAGCATCTGCTCTGACCCACAGCAATGGGACTTTGACTTGCCT 591

Db 137 TCAAGTGCAGTCAGCATCTGCTCTGACCCACAGCAATGGGACTTTGACTTGCCT 196

QY 592 GGTACTCTGAAGAGCCTGAAGGCC 617

Db 197 GGTACTCTGAAGAGCCTGAAGGCC 222

## RESULT 10

AG107877

LOCUS

DEFINITION Pan troglodytes DNA, clone: PTB-112N07.F, genomic survey sequence.

AG107877

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: chimboes@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.

## PRIMERS

Sequencing: -21M13

## LIBRARY

Vector : pKS145

FEATURES  
source

R.Site 1 : SacI

R.Site 2 : SacI

Location/Qualifiers

1. .677

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

/clone="PTB-112N07.F"

/sex="male"

/cell\_type="lymphoblast"

/clone\_lib="PTB Chimpanzee Male BAC Library"

## ORIGIN

Query Match

Best Local Similarity 12.5%; Score 146; DB 29; Length 677;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 472 GGAGCTCGGTCTCTGTCAGCCATTCAAGCTATTATTGTTCCGGAGCCGACCT 531

Db 77 GGAGCTCGGTCTCTGTCAGCCATTCAAGCTATTATTGTTCCGGAGCCGACCT 136

QY 532 TCAAGTGCAGTCAGCATCTGCTCTGACCCACAGCAATGGGACTTTGACTTGCCT 591

Db 137 TCAAGTGCAGTCAGCATCTGCTCTGACCCACAGCAATGGGACTTTGACTTGCCT 196

QY 592 GGTACTCTGAAGAGCCTGAAGGCC 617

Db 197 GGTACTCTGAAGAGCCTGAAGGCC 222

## RESULT 11

BX358189/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 10299.f

Contact : Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CSODI035A801NP1.

Location/Qualifiers

1. .1201

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CSODI035YC01"

/tissue\_type="PLACENTA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match

Best Local Similarity 9.4%; Score 110; DB 13; Length 1201;

Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1059 GCCCTCTCACAGCGGGGTGATCAACGTCACCCAGGCCAGCAAGTCATCCACAGGCTT 1118
Db 811 GCCCTCTCACAGCGGGGTGATCAACGTCACCCAGGCCAGCAAGTCATCCACAGGCTT 752
QY 1119 CTTTAAATCTGCCAGTCTCTGAGAGGTCAGTAATACAACTAGTATAG 1168
Db 751 CTTTAAATCTGCCAGTCTCTGAGAGGTCAGTAATACAACTAGTATAG 702

RESULT 12
LOCUS N47851 195 bp mRNA linear EST 14-FEB-1996
DEFINITION yw9sh05.r1 Soares_placenta 8to9weeks 2NDHP8to9W Homo sapiens cDNA
clone IMAGE:260025 5', mRNA sequence.
ACCESSION N47851
VERSION N47851.1 GI:1189017
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 185)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevisakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: T7
High quality sequence stop: 150.
FEATURES
source
1..185
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3889731"
/db_xref="taxon:9606"
/clone="IMAGE:260025"
/dev_stage="Two placentae; one from 8 weeks and another
from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_placenta 8to9weeks 2NDHP8to9W"
/notes="Organ: placenta; Vector: pT7u3D (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCGATTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."

ORIGIN
Query Match 8.6%; Score 100; DB 14; Length 185;
Best Local Similarity 100.0%; Pred. No. 3e-38;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1069 CCAGCGGGCTGATCAAGTCCACCCAGGCCAGCAAGTCATCCACAGGCTTCTTTTAACT 1128
Db 73 CCAGCGGGCTGATCAAGTCCACCCAGGCCAGCAAGTCATCCACAGGCTTCTTTTAACT 132
QY 1129 GGCCAGTCTCTGAGAAGTTCAGTAATACAACTAGTATAG 1168
Db 133 GGCCAGTCTCTGAGAAGTTCAGTAATACAACTAGTATAG 172

RESULT 14
LOCUS AQ403719 525 bp DNA linear GSS 13-MAR-1999
DEFINITION HS 5049 A1 C11 T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=625 Col=21 Row=E, genomic survey sequence.

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RESULT 13
LOCUS N93995 234 bp mRNA linear EST 05-APR-1996
DEFINITION zae6f09.r1 Soares_fetal_lung NbHL19W Homo sapiens cDNA clone
IMAGE:297545 5', mRNA sequence.
ACCESSION N93995
VERSION N93995.1 GI:1266304
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 234)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevisakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 159.
FEATURES
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1..234
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1242467"
/db_xref="taxon:9606"
/clone="IMAGE:297545"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_lung NbHL19W"
/notes="Organ: lung; Vector: pT7u3D (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGCGCAATTTTTTTTTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NbHL19W."

ORIGIN
Query Match 8.6%; Score 100; DB 14; Length 234;
Best Local Similarity 100.0%; Pred. No. 3.2e-38;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1069 CCAGCGGGCTGATCAAGTCCACCCAGGCCAGCAAGTCATCCACAGGCTTCTTTTAACT 1128
Db 113 CCAGCGGGCTGATCAAGTCCACCCAGGCCAGCAAGTCATCCACAGGCTTCTTTTAACT 172
QY 1129 GGCCAGTCTCTGAGAAGTTCAGTAATACAACTAGTATAG 1168
Db 173 GGCCAGTCTCTGAGAAGTTCAGTAATACAACTAGTATAG 212

RESULT 14
LOCUS AQ403719 525 bp DNA linear GSS 13-MAR-1999
DEFINITION HS 5049 A1 C11 T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=625 Col=21 Row=E, genomic survey sequence.

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ACCESSION      AQ403719
VERSION        AQ403719.1  GI:4414499
KEYWORDS       GSS.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1 (bases 1 to 525)
AUTHORS        Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
                Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                Hood,L.
TITLE          Sequence-tagged connectors: A sequence approach to mapping and
                scanning the human genome
JOURNAL        Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE        99380589
PUBMED         10449764
COMMENT        Contact: Mahairas GG, Wallace JC, Hood L
                High Throughput Sequencing Center
                University of Washington
                401 Queen Anne Avenue North, Seattle, WA 98109, USA
                Tel: (206) 616-3618
                Fax: (206) 616-3887
                Email: jwallace@u.washington.edu
                Clones are derived from the human BAC library RPCI-11. For BAC
                library availability, please contact Pieter de Jong
                (pieter@dejong.med.buffalo.edu). Clones may be purchased from
                BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
                or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                http://www.htsc.washington.edu
                Plate: 625 row: E column: 21
                Seq primer: T7
                Class: BAC ends
                High quality sequence stop: 525.
FEATURES       Location/Qualifiers
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                 /mol_type="genomic DNA"
                 /db_xref="taxon:9606"
                 /clone="plate=625 Col=21 Row=E"
                 /sex="male"
                 /clone_lib="RPCI-11 Human Male BAC Library"
                 /notes="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;
                 Male blood DNA was isolated from one randomly chosen donor
                 and partially digested with a combination of EcoRI and
                 EcoRI Methylase. Size selected DNA was cloned into the
                 pBACE3.6 vector at EcoRI sites"
ORIGIN
Query Match      6.5%; Score 76; DB 28; Length 525;
Best Local Similarity 100.0%; Pred. No. 3.2e-26;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1093 CAGCCAGAGTCATCCAGGCTTCTTTTAACTGCGCCAGTCTCCAGAGGTCAGTAA 1152
      |||||
Db 347 CAGCCAGCAGAGTCATCCAGGCTTCTTTTAACTGCGCCAGTCTCCAGAGGTCAGTAA 288
      |||||

QY 1153 TACAACTGTAGTATAG 1168
      |||||
Db 287 TACAACTGTAGTATAG 272
      |||||

RESULT 15
LOCUS          CK230652              976 bp      mRNA      linear      EST 09-DEC-2003
DEFINITION    ILLUMIGEN MCQ 1006 Katze_MNPL2 Macaca mulatta cDNA 5' similar to
                human LOC150084 (Hs.422120), mRNA sequence.
ACCESSION     CK230652
VERSION       CK230652.1  GI:39636835
KEYWORDS      EST.
SOURCE        Macaca mulatta (rhesus monkey)
ORGANISM      Macaca mulatta
                Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

```

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Cercopithecinae; Macaca.  
1 (bases 1 to 976)  
Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.  
Large-scale Rhesus Macaque cDNA Sequencing  
Unpublished (2003)  
Contact: C. Magness  
Illumigen Biosciences Inc.  
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
Tel: 2063780400  
Fax: 2063780408  
Email: cmagness@illumigen.com  
Sequenced on 2003.10.16. 695 020 bases. Assemblies in contig w/ 1  
member(s). Contig contains 1 (0%) lib members.

PCR Primers  
FORWARD: CCTCACTAAAGGGAACAAA  
BACKWARD: CACTATAGGCGAATTGGTA  
Insert Length: 976 Std Error: 0.00  
Plate: CL000009 row: C column: 07  
Seq primer: CCTCACTAAAGGGAACAAA  
POLYA=NO.

FEATURES  
source

Location/Qualifiers  
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/organism="Macaca mulatta"  
/mol\_type="mRNA"  
/strain="indian"  
/db\_xref="taxon:9544"  
/sex="male"  
/dev\_stage="newborn infant"  
/lab\_host="E. coli SOLR"  
/clone\_lib="Katze\_MNPL2"  
/notes="Organ: placenta; Vector: Uni-ZAP XR; Site 1: EcoR  
I; Site 2: Xho I; Created from Stratagene ZAP-CDNA  
Synthesis kit (catalog #200400) and ZAP-CDNA Gigapack III  
Gold Cloning Kit (Catalog #200450)"

ORIGIN

Query Match 5.4%; Score 63; DB 14; Length 976;  
Best Local Similarity 100.0%; Pred. No. 1.1e-19;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 285 AGCCCACTGATTCGGGAACATCAGATGCAGCCTCCAGAACAGTCGCGCTCATGATCTG 344  
 |||||  
Db 581 AGCCCACTGATTCGGGAACATCAGATGCAGCCTCCAGAACAGTCGCGCTCATGATCTG 640  
 |||||  
QY 345 CTT 347  
 |||  
Db 641 CTT 643

Search completed: September 15, 2004, 06:43:44  
Job time : 3427.42 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 22:59:39 ; Search time 3637.63 Seconds  
(without alignments)  
10179.449 Million cell updates/sec

Title: US-09-729-264-5  
Perfect score: 1240  
Sequence: 1 aggtgtgagtcgacgcaaca.....gtaatacaactgtagtag 1240

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55024014

Minimum DB seq length: 16

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST.\*

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2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_esttc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pug:*
27: em_gss_vri:*
28: gb_gsl1:*
29: gb_gsl2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	614	49.5	1201	13 BX399881	BX399881 BX399881
2	504	40.6	917	13 BX370118	BX370118 BX370118
3	447	36.0	1201	13 BX358190	BX358190 BX358190
4	443	35.7	941	13 BX403420	BX403420 BX403420

5	336	27.1	970	13	BX370209
6	226	18.2	1148	13	BX370210
7	216	17.4	725	12	BG740428
8	149	12.0	216	12	BG206666
9	146	11.8	622	29	AG069679
10	146	11.8	677	29	AG107877
11	110	8.9	1201	13	BX358189
12	100	8.1	185	14	N47851
13	100	8.1	234	14	N93995
14	80	6.5	1201	13	BX396896
15	76	6.1	525	28	AQ03719
16	63	5.1	976	14	CK230652
17	45	3.6	983	14	CK230612
18	34	2.7	527	10	BE032610
19	33	2.7	685	29	AG142221
20	32	2.6	1201	13	BX396897
21	27	2.2	565	14	CD344913
22	25	2.0	228	29	CE729707
23	25	2.0	635	28	AQ541776
24	25	2.0	834	29	CC588638
25	24	1.9	68	29	AB082057
26	23	1.9	680	9	AA941851
27	23	1.9	219	13	BQ62485
28	23	1.9	291	28	AZ411779
29	23	1.9	316	13	BQ64023
30	23	1.9	631	10	BB663870
31	23	1.9	664	28	BH020641
32	23	1.9	721	28	AQ316148
33	23	1.9	773	14	CB648901
34	23	1.9	784	12	BG863468
35	23	1.9	794	10	BF784177
36	23	1.9	824	28	BZ842183
37	23	1.9	1510	11	AK086973
38	22	1.8	167	29	CG475380
39	22	1.8	171	29	CG480695
40	22	1.8	186	13	BQ134412
41	22	1.8	198	29	CG480560
42	22	1.8	219	29	CG479279
43	22	1.8	223	29	CG615044
44	22	1.8	232	29	CG481750
45	22	1.8	234	29	CG481764

## ALIGNMENTS

## RESULT 1

BX399881

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BX399881 1201 bp mRNA linear EST 13-MAY-2003  
BX399881 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
Clone CS0D1085YA24 5-PRIME, mRNA sequence.

BX399881

EST.

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EST.

1 (bases 1 to 1201)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)

Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 10299.f, and  
it belongs to a clone representative of this cluster. For more  
information about this cluster and the virtual cDNA, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0D1085BA120P1&cluster=10299.f. Contact :

Feng Liang Email : fliang@lifetech.com URL :

BX370209 BX370209  
BX370210 BX370210  
BG740428 BG2633817  
BG206666 RST26117  
AG069679 Pan trogl  
AG107877 Pan trogl  
BX358189 BX358189  
N47851 YW95H05.r1  
N93995 za66f09.r1  
BX396896 BX396896  
AQ03719 HS\_5049 A  
CK230652 ILUMIGEN  
CK230612 ILUMIGEN  
BE032610 132035 MA  
AG142221 Pan trogl  
BX396897 BX396897  
CD344913 EtESTee75  
CE729707 tigr-988-  
AQ541776 RCI-11-3  
CC588638 CH240\_387  
AB082057 Drosophila  
AA941851 LD27161.5  
BQ62485 QG21D13.  
AZ411779 IM0185B04  
BQ64023 QSC25108.  
BB663870 BB663870  
BH020641 L8612a.d  
AQ316148 RPC11-10  
CB648901 OSJNB121  
BG863468 602796941  
BF784177 602108039  
BZ842183 CH240\_213  
CG475380 OST12736  
CG480695 OST12736  
BQ134412 1091016H0  
CG480560 OST12523  
CG479279 OST9980 M  
CG615044 OST303854  
CG481750 OST14380  
CG481764 OST14399

http://fulllength.invitrogen.com/ InvitroGen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0D1085BA12QPI.  
Location/Qualifiers  
1. .1201  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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/tissue="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES  
source

ORIGIN

Query Match 49.5%; Score 614; DB 13; Length 1201;  
Best Local Similarity 100.0%; Pred. No. 1.3e-294;  
Matches 614; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 117 GTTCTGGGTCTGTAATGAAGTCATAGAAGGCCCCCAGAAATGCAACAGTCCTGAAGGGCT 176  
Db  
272 GTTCTGGGTCTGTAATGAAGTCATAGAAGGCCCCCAGAAATGCAACAGTCCTGAAGGGCT 331  
QY 177 CCCAGGTCGCTTCACTGACCGTCTCCAGGCTGGAAGCTCATCATGTGGGCTCTCA 236  
Db  
332 CCCAGGTCGCTTCACTGACCGTCTCCAGGCTGGAAGCTCATCATGTGGGCTCTCA 391  
QY 237 GTGACATGTTGGTGTAAAGCGTCAGGCCCATGAGGCCCATCATCAATGACCGCTTCA 296  
Db  
392 GTGACATGTTGGTGTAAAGCGTCAGGCCCATGAGGCCCATCATCAATGACCGCTTCA 451  
QY 297 CCTCTCAGAGGTACGACAGCGGGGGAACCTTCACTCGGAGATGATCCCAATGTGG 356  
Db  
452 CCTCTCAGAGGTACGACAGCGGGGGAACCTTCACTCGGAGATGATCCCAATGTGG 511  
QY 357 AGCCAGTGATTCCGGGAACATCAGATGACAGCTCCAGAACAGTCGCTGCATGGATCTG 416  
Db  
512 AGCCAGTGATTCCGGGAACATCAGATGACAGCTCCAGAACAGTCGCTGCATGGATCTG 571  
QY 417 CTTAACCTTACCGTCCCAAGTTATGGGAGAGCTGTTCAATCCAGTGTAAATCTTGTAGTCG 476  
Db  
572 CTTAACCTTACCGTCCCAAGTTATGGGAGAGCTGTTCAATCCAGTGTAAATCTTGTAGTCG 631  
QY 477 CTGAGATGAACCTTGTGAAGTACTTGTCTACCTCAGCTGACCCGCGCTCCCGGATA 536  
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632 CTGAGATGAACCTTGTGAAGTACTTGTCTACCTCAGCTGACCCGCGCTCCCGGATA 691  
QY 537 TTTCTCGGAGCTCGGTCTCCTGCTCAGCCATTCAGCTATTAATTTTGTTCGGAGCCCA 596  
Db  
692 TTTCTCGGAGCTCGGTCTCCTGCTCAGCCATTCAGCTATTAATTTTGTTCGGAGCCCA 751  
QY 597 GCGACCTTCAAAGTGCAGTGAAGCATCTGGCTGTGACCCCAACAGAAATGGGACTTTGA 656  
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752 GCGACCTTCAAAGTGCAGTGAAGCATCTGGCTGTGACCCCAACAGAAATGGGACTTTGA 811  
QY 657 CTTGCGTGGCTACCTTGAAGAGCTGAAGGCGCGCAAGTCTGCACTGTAAATCTCACTG 716  
Db  
812 CTTGCGTGGCTACCTTGAAGAGCTGAAGGCGCGCAAGTCTGCACTGTAAATCTCACTG 871  
QY 717 TGATTTCGTTGCTCC 730  
Db 872 TGATTTCGTTGCTCC 885

RESULT 2  
BX370118 917 bp mRNA linear EST 08-MAY-2003  
LOCUS BX370118 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
DEFINITION clone CS0D1076YN22 5-PRIME, mRNA sequence.  
ACCESSION BX370118  
VERSION BX370118.1 GI:30447910  
KEYWORDS EST.

SOURCE  
ORGANISM

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 917)  
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by life technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 2250.r For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0BAG037ZE05 CS03493\_2&cluster=2250.r.  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0BAG037ZE05\_CS03493\_2.  
Location/Qualifiers  
1. .917  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
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/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES  
source

1. .917  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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/tissue type="PLACENTA COT 25-NORMALIZED"  
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primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 40.6%; Score 504; DB 13; Length 917;  
Best Local Similarity 100.0%; Pred. No. 9.1e-240;  
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 737 ACTGGAGGTGGTATTATATTCAGGTGTATTATCAAGTTTACGAGTTAGGTTTTCA 796  
Db  
31 ACTGGAGGTGGTATTATATTCAGGTGTATTATCAAGTTTACGAGTTAGGTTTTCA 90  
QY 797 TTGCTTACTTGGGGCAAGTTGGACTTGGACTAGCAGCACCATTCTTGACCCGACG 856  
Db  
91 TTGCTTACTTGGGGCAAGTTGGACTTGGACTAGCAGCACCATTCTTGACCCGACG 150  
QY 857 TGTACTCTTACAATACGCTGCTGCTGCGCGCTGTTGTTGTTGCTGCAACTGCTGC 916  
Db  
151 TGTACTCTTACAATACGCTGCTGCTGCGCGCTGTTGTTGTTGCTGCAACTGCTGC 210  
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211 TGCGGTTGTTGTTTCTGCTGTAGAAGAAAAGAGATTCGTATTCATTTCAAAAGAAA 270  
QY 977 TCTGAAAAGAGAAGACAAACAAAGAACTGAGACAGAAATGAAATGAAATCTCCGC 1036  
Db  
271 TCTGAAAAGAGAAGACAAACAAAGAACTGAGACAGAAATGAAATGAAATCTCCGC 330  
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331 TACAATTCAGATGAACAAAAGACCAAGAACCCGCTTCTCTCCCTCCCAATCTCTGTAA 390  
QY 1097 TCCAGTGATCTGAACAAAGAAAAGTAGCTGTGGCCCTCTCTACAGCGGGCTGATCAA 1156  
Db  
391 TCCAGTGATCTGAACAAAGAAAAGTAGCTGTGGCCCTCTCTACAGCGGGCTGATCAA 450  
QY 1157 CGTCCACCCAGCGCAGCAAGTCATCCACAGGCTTCTTTAATCTGGCCAGTCTGAGAAG 1216  
Db  
451 CGTCCACCCAGCGCAGCAAGTCATCCACAGGCTTCTTTAATCTGGCCAGTCTGAGAAG 510  
QY 1217 GTCAGTAATACAACCTGTAGTATAG 1240  
Db 511 GTCAGTAATACAACCTGTAGTATAG 534



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RESULT 3
BX358190
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10299.f
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DI035AB01QPI.
Location/Qualifiers
1. 1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI035YC01"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dt)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
FEATURES
source
Query Match 36.0%; Score 447; DB 13; Length 1201;
Best Local Similarity 99.8%; Pred. No. 2.6e-211;
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 743 GGTGGTATTATATTCAGGTGATTATCAAGTTTACCGAGTTTAGGTTTTCATTGCGCT 802
DB 64 GGTGGTATTATATTCAGGTGATTATCAAGTTTACCGAGTTTAGGTTTTCATTGCGCT 123
QY 803 ACTTGGGGGAAAGTTGGACTTGGACTAGGACGACGATGCTTCTGACGCCGACGTGTACT 862
DB 124 ACTTGGGGGAAAGTTGGACTTGGACTAGGACGACGATGCTTCTGACGCCGACGTGTACT 183
QY 863 CTTTACAAATACGCTGCTGCTGCTGCGCGCGTGTGTTGTTGCTGCACTGCTGCGCT 922
DB 184 CTTTACAAATACGCTGCTGCTGCTGCGCGCGTGTGTTGTTGCTGCACTGCTGCGCT 243
QY 923 TGTGTTTCTGCTGTAGAGAAAGAGGATTTTCGTAATTCATTTCAAAAGAAATCTGAA 982
DB 244 TGTGTTTCTGCTGTAGAGAAAGAGGATTTTCGTAATTCATTTCAAAAGAAATCTGAA 303
QY 983 AAAGAGACAAACAAAGAACTGAGACAGAAAGTGGAAATGAAACTCCGCTACAAT 1042
DB 304 AAAGAGACAAACAAAGAACTGAGACAGAAAGTGGAAATGAAACTCCGCTACAAT 363
QY 1043 TCAGATGAACAAAGAACCAAGAAACCGCTTCTCCCTCCCAAACTCCGCTACAAT 1102
DB 364 TCAGATGAACAAAGAACCAAGAAACCGCTTCTCCCTCCCAAACTCCGCTACAAT 423
QY 1103 GATCTTGAACAAAGAAACAGTAGCTGTGGCCCTCTCCCTCACCAGCGGCTGATCAAGTCCA 1162
DB 424 GATCTTGAACAAAGAAACAGTAGCTGTGGCCCTCTCCCTCACCAGCGGCTGATCAAGTCCA 483

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QY 1163 CCCAGCCAGCAAGTCATCCACAGGCTCTTTTAACTCTGGCCAGTCTCTGAGAGGTCACT 1222
DB 484 CCCAGCCAGCAAGTCATCCACAGGCTCTTTTAACTCTGGCCAGTCTCTGAGAGGTCACT 543
QY 1223 AATACAACCTGTAGTATAG 1240
DB 544 AATACAACCTGTAGTATAG 561
RESULT 4
BX403420
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 941)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
10299.f, and it belongs to a clone representative of this cluster.
For more information about this cluster and the virtual cDNA, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS5AA017ZE02RM1&cluster=10299.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS5AA017ZE02RM1.
Location/Qualifiers
1. 941
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI085YA24"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dt)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
FEATURES
source
Query Match 35.7%; Score 443; DB 13; Length 941;
Best Local Similarity 100.0%; Pred. No. 2.5e-209;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 117 GTTCTGGGCTCTGGTATGAAGTCATAGAGGCCCCCAGAAATGCAACAGTCTGAGAGGCT 176
DB 286 GTTCTGGGCTCTGGTATGAAGTCATAGAGGCCCCCAGAAATGCAACAGTCTGAGAGGCT 345
QY 177 CCAGGCTCGCTTCAACTGACCGTCTCCAGGGCTGGAGGCTCATCATGTGGGCTCTCA 236
DB 346 CCAGGCTCGCTTCAACTGACCGTCTCCAGGGCTGGAGGCTCATCATGTGGGCTCTCA 405
QY 237 GTGACATGGTGGTGTAGCGTCAAGGCCCATGAGGCCCATCATCAATGACCGCTTCA 296
DB 406 GTGACATGGTGGTGTAGCGTCAAGGCCCATGAGGCCCATCATCAATGACCGCTTCA 465
QY 297 CCTCTCAGAGGTACGACAGCGGGGAACTTCACTCGGAGATGATCATCAATGTGG 356
DB 466 CCTCTCAGAGGTACGACAGCGGGGAACTTCACTCGGAGATGATCATCAATGTGG 525
QY 357 AGCCCCAGTGATTGGGGGAACATCATGAGCGCTTCAGAACAGTGCCTGCATGATCTG 416

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Db 526 AGCCAGTGATTCGGGGAACATCAGATGAGCCTCAGAACAGTCGCCCTGATGATCTG 585  
Qy 417 CTACCTTACCGTCCAGGTTATGGAGAGCTGTTCAITCCCAGTGTAAATCTTGTAGTCG 476  
Db 586 CTACCTTACCGTCCAGGTTATGGAGAGCTGTTCAITCCCAGTGTAAATCTTGTAGTCG 645  
Qy 477 CTGAGAAATGAACCTTGTGAAGTTACTTGTCTACCTCAGTGGACCGGCTCCCGGATA 536  
Db 646 CTGAGAAATGAACCTTGTGAAGTTACTTGTCTACCTCAGTGGACCGGCTCCCGGATA 705  
Qy 537 TTTCCTGGAGCTCGGTCCTCG 559  
Db 706 TTTCCTGGAGCTCGGTCCTCG 728

RESULT 5  
BX370209  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BX370209 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CS0D1085YA24 5-PRIME, mRNA sequence.  
BX370209  
BX370209.1 GI:30451880  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 970)  
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 10299.f, and  
it belongs to a clone representative of this cluster. For more  
information about this cluster and the virtual cDNA, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0BAG039ZE05\_CS03685\_1&cluster=10299.f.  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0BAG039ZE05\_CS03685\_1.  
Location/Qualifiers  
1. .970  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0D1085YA24"  
/tissue type="PLACENTA COT 25-NORMALIZED"  
/note="First strand cDNA was primed with a NotI-oligo (dr)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES  
source  
1. .970  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0D1085YA24"  
/tissue type="PLACENTA COT 25-NORMALIZED"  
/note="First strand cDNA was primed with a NotI-oligo (dr)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
Query Match 27.1%; Score 336; DB 13; Length 970;  
Best Local Similarity 100.0%; Pred. No. 5.9e-156;  
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 738 CTGAGGTTGGTATTATATCCAGGTGATTTATCAAGTTTACCGAGTTTATGTTTTCAT 797  
Db 32 CTGAGGTTGGTATTATATCCAGGTGATTTATCAAGTTTACCGAGTTTATGTTTTCAT 91  
Qy 798 TGCCTACTTGGGCAAGTTGGACTTGGACTAGCAGGACCATGTTCTGACCGCAGCT 857  
Db 92 TGCCTACTTGGGCAAGTTGGACTTGGACTAGCAGGACCATGTTCTGACCGCAGCT 151  
Qy 858 GTACTCTTACAAATACGCTGCTGCTGCCCGCTGTTGTTGCTGCTCAATCTGCTGCT 917

Db 152 GTACTCTTACAAATACGCTGCTGCTGCCCGCTGTTGTTGCTGCTGCTGCTGCT 211  
Qy 918 GCCGTTGTTGTTTCTGCTGTAGAGAAAAGAGAGATTTTCGATTCAATTTCAAAAAGAAAT 977  
Db 212 GCCGTTGTTGTTTCTGCTGTAGAGAAAAGAGAGATTTTCGATTCAATTTCAAAAAGAAAT 271  
Qy 978 CTGAAAAAGAGAGACAAACAAAGAACTGAGACAGAAAGTGAATGAATACTCCGCT 1037  
Db 272 CTGAAAAAGAGAGACAAACAAAGAACTGAGACAGAAAGTGAATGAATACTCCGCT 331  
Qy 1038 ACAATTCAGATCAACAAAAGAACCCACAGAAACCGCTT 1073  
Db 332 ACAATTCAGATCAACAAAAGAACCCACAGAAACCGCTT 367

RESULT 6  
BX370210  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BX370210 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CS0D1085YA24 5-PRIME, mRNA sequence.  
BX370210  
BX370210.1 GI:30451881  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1148)  
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 10299.f, and  
it belongs to a clone representative of this cluster. For more  
information about this cluster and the virtual cDNA, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0BAG039ZE05\_CS03685\_2&cluster=10299.f.  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Paraday Avenue Genoscope sequence ID : CS0BAG039ZE05\_CS03685\_2.  
Location/Qualifiers  
1. .1148  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0D1085YA24"  
/tissue type="PLACENTA COT 25-NORMALIZED"  
/note="First strand cDNA was primed with a NotI-oligo (dr)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES  
source  
1. .1148  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0D1085YA24"  
/tissue type="PLACENTA COT 25-NORMALIZED"  
/note="First strand cDNA was primed with a NotI-oligo (dr)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
Query Match 18.2%; Score 226; DB 13; Length 1148;  
Best Local Similarity 100.0%; Pred. No. 4.6e-101;  
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 730 CCAAGACACTGGAGTGGTATTAATATTCAGAGTGTATATCAAGTTTACCGAGTTTAGG 789  
Db 14 CCAAGACACTGGAGTGGTATTAATATTCAGAGTGTATATCAAGTTTACCGAGTTTAGG 73  
Qy 790 TTTTTCATTCGCTACTTCGGGCAAGTTGGACTTGGACTAGCAGGACCATGTTCTGAC 849  
Db 74 TTTTTCATTCGCTACTTCGGGCAAGTTGGACTTGGACTAGCAGGACCATGTTCTGAC 133  
Qy 850 GCCGACGTTGTTACTTCTTACAATAACGCTGCTGCTGCCCGCTGTTGTTGCTGCTGCA 909  
Db 134 GCCGACGTTGTTACTTCTTACAATAACGCTGCTGCTGCCCGCTGTTGTTGCTGCTGCA 193

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QY 910 CTGCTGCTGCCGTTGTTGTTCTGCTGTAGAGAAAAAGAGGATTT 955
Db |||||||
194 TGCCTGCTGCCGTTGTTGTTCTGCTGTAGAGAAAAAGAGGATTT 239
|||

RESULT 7
LOCUS BG740428 725 bp mRNA linear EST 15-MAY-2001
DEFINITION 6026381.F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:477879 5',
ACCESSION BG740428 mRNA sequence.
VERSION BG740428.1 GI:14051081
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 725)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999);
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10635 row: b column: 06
High quality sequence stop: 725.
FEATURES
source
1. 725
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4778789"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Skn3"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Query Match 17.4%; Score 216; DB 12; Length 725;
Best Local Similarity 99.6%; Pred. No. 4.1e-96;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 973 GAAATCTGAAAAAGAGAAGACAAACAAAGAACTGTGACAGACAAAGTGAATGAAACTC 1032
Db |||||||
379 GAAATCTGAAAAAGAGAAGACAAACAAAGAACTGTGACAGACAAAGTGAATGAAACTC 438
|||

QY 1033 CGSCTACAATTCAGATGACAAAGAACCAAGAAACCGCTTCTCTCCCTCCCAAACTCTG 1092
Db |||||||
439 CGSCTACAATTCAGATGACAAAGAACCAAGAAACCGCTTCTCTCCCTCCCAAACTCTG 498
|||

QY 1093 TGAATCCAGTGTATCTTGAACAAAGAAACAGTAGCTGTGCGCTCTCTCCAGCGGGCTGA 1152
Db |||||||
499 TGAATCCAGTGTATCTTGAACAAAGAAACAGTAGCTGTGCGCTCTCTCCAGCGGGCTGA 558
|||

QY 1153 TCAAGTCCACCCAGCGCCAGCAAGTCATCCACAGGCTTCTTTTAATCTGCCAGTCTCTGA 1212
Db |||||||
559 TCAAGTCCACCCAGCGCCAGCAAGTCATCCACAGGCTTCTTTTAATCTGCCAGTCTCTGA 618
|||

QY 1213 GAAGGTCAATAACAATCTGTAGTATA 1239
Db |||||||
619 GAAGGTCAATAACAATCTGTAGTATA 645
|||

RESULT 8
LOCUS AG069679 622 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-060F12.F, genomic survey sequence.
ACCESSION AG069679
VERSION AG069679.1 GI:16621481
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

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BG206666
LOCUS RST26117 Achersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG206666
VERSION BG206666.1 GI:13728353
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 216)
AUTHORS Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R.,
Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S.,
Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K.,
Offenbacher, J., Danzig, J. and Ducar, M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
JOURNAL 21227151
MEDLINE 11329013
PUBMED
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave., Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 166.
FEATURES
source
1. 216
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
ORIGIN
Query Match 12.0%; Score 149; DB 12; Length 216;
Best Local Similarity 100.0%; Pred. NO. 8.1e-63;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1083 CCAATCTCTGTGAATCCAGTGATCCTGCAACAAAGAAACAGTAGTGCGCCCTCCTCACC 1142
Db |||||||
21 CCAATCTCTGTGAATCCAGTGATCCTGCAACAAAGAAACAGTAGTGCGCCCTCCTCACC 80
|||

QY 1143 AGCGGCTGATCAACGTCCACCCAGCGCAAGTCATCCACAGGCTCTCTTTAATCTGG 1202
Db |||||||
81 AGCGGCTGATCAACGTCCACCCAGCGCAAGTCATCCACAGGCTCTCTTTAATCTGG 140
|||

QY 1203 CCAGTCTCTGAGAAGTCAAGTATACAACT 1231
Db |||||||
141 CCAGTCTCTGAGAAGTCAAGTATACAACT 169
|||

RESULT 9
LOCUS AG069679
DEFINITION Pan troglodytes DNA, clone: PTB-060F12.F, genomic survey sequence.
ACCESSION AG069679
VERSION AG069679.1 GI:16621481
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

```



digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 3.5e-43; Length 1201;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1131 GCCCTCTCCACAGCGGCTGATCAACGTCACCCAGGCGCCAGCAAGTCATCCACAGGCTT 1190
Db 811 GCCCTCTCCACAGCGGCTGATCAACGTCACCCAGGCGCCAGCAAGTCATCCACAGGCTT 752

QY 1191 CTTTAAATCTGCCAGTCTCCTGAGAGGTCAGTAATACAACTGTAGTATAG 1240
Db 751 CTTTAAATCTGCCAGTCTCCTGAGAGGTCAGTAATACAACTGTAGTATAG 702

RESULT 12
LOCUS N47851 185 bp mRNA linear EST 14-FEB-1996
DEFINITION YW95h05.r1 Soares_placenta 8to9weeks 2NBHP8to9W Homo sapiens cDNA
ACCESSION N47851
VERSION N47851.1 GI:1189017
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 185)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: T7
High quality sequence stop: 150.
FEATURES
source
1..185
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3889731"
/db_xref="taxon:9606"
/clone="IMAGE:260025"
/dev_stage="two placentae; one from 8 weeks and another from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_placenta 8to9weeks 2NBHP8to9W"
/notes="Organ: placenta; Vector: p77n3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo (dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p77n3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e-38; Length 185;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1141 CCAGCGGGCTGATCAACGTCACCCAGGCGCCAGCAAGTCATCCACAGGCTTCTTTTAATCT 1200
Db 73 CCAGCGGGCTGATCAACGTCACCCAGGCGCCAGCAAGTCATCCACAGGCTTCTTTTAATCT 132

QY 1201 GGCCAGTCTCTGAGAAGGTCAGTAATACAACTGTAGTATAG 1240
Db 133 GGCCAGTCTCTGAGAAGGTCAGTAATACAACTGTAGTATAG 172

RESULT 13
LOCUS N93995 234 bp mRNA linear EST 05-APR-1996
DEFINITION za66f09.r1 Soares fetal lung NBHL19W Homo sapiens cDNA clone
ACCESSION N93995
VERSION N93995.1 GI:1266304
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 234)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 159.
FEATURES
source
1..234
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1242467"
/db_xref="taxon:9606"
/clone="IMAGE:297545"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_lung NBHL19W"
/notes="Organ: lung; Vector: p77n3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo (dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p77n3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBHL19W."

ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-38; Length 234;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1141 CCAGCGGGCTGATCAACGTCACCCAGGCGCCAGCAAGTCATCCACAGGCTTCTTTTAATCT 1200
Db 113 CCAGCGGGCTGATCAACGTCACCCAGGCGCCAGCAAGTCATCCACAGGCTTCTTTTAATCT 172

QY 1201 GGCCAGTCTCTGAGAAGGTCAGTAATACAACTGTAGTATAG 1240
Db 133 GGCCAGTCTCTGAGAAGGTCAGTAATACAACTGTAGTATAG 172

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Db 173 GCCAGTCTCGAAGGTCAGTATACAACTGTAGTATAG 212

RESULT 14  
BX396896/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1201 bp mRNA linear EST 13-MAY-2003  
BX396896 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CS0D1026Y017 3-PRIME, mRNA sequence.  
BX396896  
BX396896.1 GI:306113250  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1201)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 10238.f, and  
it belongs to a clone representative of this cluster. For more  
information about this cluster and the virtual cDNA, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0D1026AH09NP1&cluster=10298.f. Contact :  
Peng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Paradise Avenue Genoscope sequence ID : CS0D1026AH09NP1.  
Location/Qualifiers  
1. 1201  
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/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(GT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES  
source  
1. 525  
/organism="Homo sapiens"  
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/clone="Plate=625 Col=21 Row=E"  
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/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRI Methylase. Size selected DNA was cloned into the  
pBACe3.6 vector at EcoRI sites"

ORIGIN  
Query Match 6.1%; Score 76; DB 28; Length 525;  
Best Local Similarity 100.0%; Pred. No. 2.6e-26;  
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Qy 1165 CAGCCAGCAGTCATCCACGAGCTCTTTTAACTCGCCAGTCCTCAGAGGTCAGTAA 1224  
Db 347 CAGCCAGCAGTCATCCACGAGCTCTTTTAACTCGCCAGTCCTCAGAGGTCAGTAA 288  
Qy 1225 TACAACTGTAGTATAG 1240  
Db 287 TACAACTGTAGTATAG 272

Search completed: September 15, 2004, 06:43:45  
Job time : 3638.63 secs

Db 173 GCCAGTCTCGAAGGTCAGTATACAACTGTAGTATAG 212

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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

525 bp DNA linear GSS 13-MAR-1999  
HS\_5049\_Ai\_C11\_T7A RPCI-11 Human Male BAC Library Homo sapiens  
genomic clone Plate=625 Col=21 Row=E, genomic survey sequence.  
AQ403719  
AQ403719  
AQ403719.1 GI:4414499  
GSS.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 525)  
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,

Query Match 6.5%; Score 80; DB 13; Length 1201;  
Best Local Similarity 100.0%; Pred. No. 3.2e-28;  
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Db 726 AGGTGTGAGTCCAGCCACAGTCGTGGATTCAGTTTCCTAGGTCGCATACAAAGCACCAT 667  
Qy 61 AACCTGGTGGCTTAGACAA 80  
Db 666 AACCTGGTGGCTTAGACAA 647

RESULT 15  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

525 bp DNA linear GSS 13-MAR-1999  
HS\_5049\_Ai\_C11\_T7A RPCI-11 Human Male BAC Library Homo sapiens  
genomic clone Plate=625 Col=21 Row=E, genomic survey sequence.  
AQ403719  
AQ403719  
AQ403719.1 GI:4414499  
GSS.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 525)  
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 20:48:25 ; Search time 4828.88 Seconds  
(without alignments)  
10546.560 Million cell updates/sec

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Sequence: 1 ctgtctgccccatctgaataa.....gtaatacaactgtagtatag 1175

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Scoring table:  OLIGO_NJC
                  Gapop 60.0 , Gapext 60.0

Searched:      3470272 seqs, 21671516995 residues

Word size :    0

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Total number of hits satisfying chosen parameters: 6784142

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Minimum DB seq length: 16
Maximum DB seq length: 2000000000
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Post-processing: Listing first 45 summaries

Database : GenEmbl:★

General:

- 1: gb\_bat.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_phi.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_to.\*
- 11: gb\_trs.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_to.\*
- 27: em\_trs.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %			DB	ID	Description
		Match	Length				
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2	1076	91.6	2051	6	AX374579	Sequence	
3	1076	91.6	2051	6	AK092516	Homo sapi	
4	1074	91.4	1240	6	AX380400	Sequence	
5	1027	87.4	1168	6	AX380398	Sequence	
6	739	62.9	1139	6	AX380402	Sequence	
7	302	25.7	142742	9	AF121782	Homo sapi	
8	302	25.7	340000	9	HS211C080	Homo sapi	
9	200	17.0	182532	9	CHI179K04	Homo sapi	
10	145	12.3	156288	9	HS000162	Pan trogl	
11	100	8.5	199665	9	AF064857	Pan trogl	
12	72	6.1	192219	9	RP43002119	Homo sapi	
13	53	4.5	42025	9	AF045450	Homo sapi	
14	53	4.5	170121	9	AF064860	Homo sapi	
15	25	2.1	6470	3	AB090820	Homo sapi	
16	24	2.0	5178	3	AX119603	Anopheles	
17	24	2.0	8152	3	DMT0C	Drosophil	
18	24	2.0	77137	3	AC004422	Drosophil	
19	24	2.0	83876	2	AC020009	Drosophil	
20	24	2.0	148102	8	AP003328	Oryza sat	
21	24	2.0	148762	8	AP002843	Oryza sat	
22	24	2.0	169931	3	AC088321	Drosophil	
23	24	2.0	184554	3	AC099022	Drosophil	
24	24	2.0	268984	3	AE001274	Leishmani	
25	24	2.0	314957	3	AE003581	Drosophil	
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27	23	2.0	1195	6	AX380404	Sequence	
28	23	2.0	29865	2	AC020047	Drosophil	
29	23	2.0	162256	3	AC108135	Leishmani	
30	23	2.0	124612	2	AC105442	Leishmani	
31	23	2.0	149964	2	AC120145	Mus muscu	
32	23	2.0	166000	3	AC104511	Drosophil	
33	23	2.0	167926	3	AC023685	Drosophil	
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36	23	2.0	136900	2	AC020851	Mus muscu	
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39	22	1.9	757	8	BT004026	Arabidops	
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41	22	1.9	1200	6	AD92049	Sequence 3	
42	22	1.9	1203	6	BD251402	Novel neu	
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LOCUS	Sequence 1104 from Patent EP1308459.		
DEFINITION	AX747579		
ACCESSION	AX747579.1	GI:32131967	
VERSION			
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	1		Isegai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and Masubo, Y.
TITLE	Full-length cDNA sequences		
JOURNAL	Patent: EP 1308459-A 1104 07-MAY-2003;		
	Helix Research Institute (JP); Research Association for Biotechnology (JP)		
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Best Local Similarity	99.9%;	Pred. No. 0;	
Matches 1126;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;
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QY	109	GCTCCAGGCTCGTTCAACTGACCGTCTCCAGGCTGGAAGCTCATCATGTGGGCTC	168
DB	261	GCTCCAGGCTCGTTCAACTGACCGTCTCCAGGCTGGAAGCTCATCATGTGGGCTC	320
QY	169	TCAGTGACATGGTGGTGAAGCGTCAGGCGCCCATGAGCCCATCATCAACATGACCGCT	238



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RESULT 3  
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LOCUS

DEFINITION Homo sapiens cDNA FLJ35197 fis, clone PLACE6017788, highly similar to IGSF5.

AK092516

2051 bp

mRNA

linear

PRI 15-JUL-2002

## ACCESSION

AK092516.1 GI:21751130

VERSION Oligo capping; fis (full insert sequence).

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Kawakami,B., Sugiyama,A., Takemoto,M., Sugiyama,T., Irie,R.,

Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,

Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,

Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,

Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,

Oshina,A., Suzuki,Y., Sugano,S., Negahari,K., Masuho,Y., Nagai,K.

and Isogai,T.

NEDO human cDNA sequencing project

Unpublished

REFERENCE 2 (bases 1 to 2051)

AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatacari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing;

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- and 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.

FEATURES

Location/Qualifiers

1..2051

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Best Local Similarity 99.9%; Pred.No.0;

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Qy 169 TCAGTGACATGTGTGTAAGCTCAGCGCCATGGAGCCCATCATCCCAATGACCGCT 228

Db 321 TCAGTGACATGTGTGTAAGCTCAGCGCCATGGAGCCCATCATCCCAATGACCGCT 380

Qy 229 TCACCTCTCAGAGGTACGACCCAGGCGGAACTTACCTCGGAGATGATCATCCCAATG 288

Db 381 TCACCTCTCAGAGGTACGACCCAGGCGGAACTTACCTCGGAGATGATCATCCCAATG 440

Qy 289 TGGAGCCAGTGAATTCGGGGAAACATCAGATGAGCGCTCCAGAAACAGTGCCTGCAATG 348

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QY	589	TGACTTGGTGGTCTACCTGGAGAGCTGAAGCCCGGCAAGTCTGCAACTGTAATCTCA	648
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QY	769	GCACCAATGTTCTGACCGCAGTGTAATCTTACAAATAGCTGCTGCTGCTGCGCGTC	828
Db	921	GCACCAATGTTCTGACCGCAGTGTAATCTTACAAATAGCTGCTGCTGCTGCGCGTC	980
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QY	1129	TTAATCTGGCAGTCTCTGAGAGGTCAGTAATCAACTGTAGTATAG	1175
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Welcher, A.A., Sarmiento, U.M., Schultz, H.J. and Chute, H.T.			
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Patent: WO 0200710-A 5 03-JAN-2002;			
Angen, Inc. (US)			
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QY	351	GCTTACCTTACCGTCCAAAGTTATGGAGAGCTGTTCAATCCCAAGTGTAACTTTAGTC	410
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QY	471	ATTTCTCTGGAGCTCGGTCTCTGCTGAGCAATCAAGCTATTATTTTTCGGAGGCC	530
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QY	531	AGCGACCTTCAAAGTCAGTGAGCATCTCGGTCTGACCCCAAGAGCAATGGACTTTG	590
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QY	591	ACTTGGTGTGCTACCTGGAAGACCTTGAAGCCGCAAGTCTGCACTGTAATCTCACT	650
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QY	831	TGTTGTGGCTGCAACTGCTGCTGCGGTGTTGTTTCTGCTGTAGAGAAAGAGGATTT	890
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QY      951  AGTGGAAATGAAATCTCCGGCTACAAATTCAGATGAAACAAAGACACACACACCGCTTCT  1010
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QY     1011  CTCCTCTCCAAATCTCTGTGAATCCAGTGTATCTCTGAAACAAAGAAACAGTAGCTGTGGCCCT  1070
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QY     1071  CCTCACCAGGGGCTGATCAACAGTCCACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  1130
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QY     1131  AATCTGGCCAGTCCCTGAGAGAGTCAAGTATACAACTGTAGTATAG  1175
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RESULT 5
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LOCUS      AX380398
DEFINITION Sequence 3 from Patent WO0200710.
ACCESSION AX380398
VERSION    AX380398.1
KEYWORDS   AX380398.1
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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AUTHORS    1
            Welcher, A.A., Sarmiento, U.M., Schultz, H.J. and Chute, H.T.
TITLE      B7-like molecules and uses thereof
JOURNAL    Patent: WO 0200710-A 3 03-JAN-2002;
            Amgen, Inc. (US)

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DEFINITION Sequence 7 from Patent WO0200710.
ACCESSION AX380402
VERSION    AX380402.1
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REFERENCE  1

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AUTHORS Welcher, A.A., Sarmiento, U.M., Schultz, H.J. and Chute, H.T.  
TITLE B7-like molecules and uses thereof  
JOURNAL Patent: WO 020710-A 7 03-JAN-2002;  
Amgen, Inc. (US)

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ORGANISM Homo sapiens  
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AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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Taudien, S., Dagand, E., Hildmann, T., Nordsiek, G., Drescher, B.,  
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Rosenthal, A.  
TITLE Direct Submission  
JOURNAL Submitted (21-JAN-1999) Genome Analysis, Institute for Molecular  
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exon               /evidence=not_experimental
4712. .4749
/note="Xpound exon prediction, score = 70% (0%)"
repeat_region      /evidence=not_experimental
5385. .6104
/evidence=not_experimental
exon               /rpt_family="HERV1"
6682. .6751
/note="MZEF, score = 95.1%"
exon               /evidence=not_experimental
6746. .6751
/note="Genscan, score = 1.83%, comment = Initial_exon 6 bp
frame: 1 phase: 0"
repeat_region      /evidence=not_experimental
6901. .7339
/rpt_family="MLT1C"
7347. .7457
/evidence=not_experimental
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/rpt_family="LRI6C"
complement(7561. .7696)
/evidence=not_experimental
repeat_region      /rpt_family="MIR"
complement(7819. .8220)
/evidence=not_experimental
exon               /rpt_family="MLT1J"
8097. .8119
/note="GRAL1, score = 45.000%, comment = marginal"
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complement(8738. .9232)
/evidence=not_experimental
exon               /rpt_family="MLT1C"
complement(9273. .9420)
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exon               /evidence=not_experimental
9290. .9371
/note="GRAL1, score = 81.000%, comment = excellent shadow"
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9966. .10041
/note="homology = 100.00%, score = 38, counts = 2"
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10244. .10664
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10665. .11028
/evidence=not_experimental
repeat_region      /rpt_family="MLT1F"
11318. .11417
/evidence=not_experimental
repeat_region      /rpt_family="LIMC/D"
11503. .11818
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complement(14962. .15036)
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/note="GRAL1, score = 66.000%, comment = good"
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 Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 368 AGTTATGGAGAGCTGTTCAATCCAGTGTAAATCTTGTAGTCGCTGAGATGAACCTTG 427  
Db 49654 AGTTATGGAGAGCTGTTCAATCCAGTGTAAATCTTGTAGTCGCTGAGATGAACCTTG 49713  
QY 428 TGAAGTTACTTGTCTACCTTCACACTGGACCCGGCTCCCGGATATTTCTCGGAGCTCGG 487  
Db 49714 TGAAGTTACTTGTCTACCTTCACACTGGACCCGGCTCCCGGATATTTCTCGGAGCTCGG 49773  
QY 488 TCTCTGGTGCAGCAATCAAGCTATTTATTTGTTCGGAGCCAGGACCTTCAAGTGC 547  
Db 49774 TCTCTGGTGCAGCAATCAAGCTATTTATTTGTTCGGAGCCAGGACCTTCAAGTGC 49833  
QY 548 AGTGAGATCCTGGCTCTGACCCACAGACCAATGGACTTTCACTTGGTGGCTACCTTG 607  
Db 49834 AGTGAGATCCTGGCTCTGACCCACAGACCAATGGACTTTCACTTGGTGGCTACCTTG 49893  
QY 608 GAAGAGCCTGAAGCCCGCAAGTCTGCAACTGTAATCTCACTGTGATTCGGTGTCCCA 667  
Db 49894 GAAGAGCCTGAAGCCCGCAAGTCTGCAACTGTAATCTCACTGTGATTCGGTGTCCCA 49953  
QY 668 AG 669  
Db 49954 AG 49955  
RESULT 8  
HS21C080 340000 bp DNA linear PRI 24-MAY-2000  
LOCUS Homo sapiens chromosome 21 segment HS21C080.  
DEFINITION AL163280 AP001735 BA000005  
ACCESSION AL163280.2 GI:7717369  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 340000)  
Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,  
Park,H.S., Toyoda,A., Ishii,K., Toriki,Y., Choi,D.K., Soeda,E.,  
Okai,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,  
Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,  
Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A.,  
Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K.,  
Aakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyama,S.,  
Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordstiek,G.,  
Hornischer,K., Brandt,P., Scharfe,M., Schoen,O., Desario,A.,  
Reichelt,J., Kauer,G., Bloecker,H., Ramser,J., Beck,A., Klages,S.,  
Hennig,S., Riesselmann,L., Degand,E., Wehrmeyer,S., Borzym,K.,  
Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and  
Yaspo,M.L.  
Direct Submission  
Submitted (05-MAY-2000) The Chromosome 21 Mapping and Sequencing  
Consortium: \* RIKEN Genomic Sciences Center, Human Genome Research  
Group \* Institute of Molecular Biotechnology, Genome Analysis \*  
Keio University School of Medicine, Dept. of Molecular Biology \*  
GBF, Dept. of Genome Analysis \* Max-Planck Institute for Molecular  
Genetics (addresses see below)  
The Chromosome 21 Mapping and Sequencing Consortium consists of  
\* RIKEN Genomic Sciences Center, Human Genome Research Group, \*  
Sagamihara 228-8555, Japan,  
\* e.mail: sakaki@gsr.riken.go.jp  
\* URL: http://hgp.gsc.riken.go.jp/  
and  
\* Institute of Molecular Biotechnology, Genome Analysis, \*  
Beutenbergstrasse 11, D-07745 Jena, Germany,  
\* e.mail: gscj-submit@genome.imb-jena.de  
\* URL: http://genome.imb-jena.de/  
and  
\* Keio University School of Medicine, Dept. of Molecular Biology, \*  
Tokyo 160-8582, Japan,  
\* e.mail: shimizumedb-med.keio.ac.jp  
\* URL: http://adenine.dmb.med.keio.ac.jp/  
and

\* GBF, Dept. of Genome Analysis,  
\* Mascheroder Weg 1, D-38124 Braunschweig, Germany, \* e.mail:  
info.genome@gbf.de  
\* URL: http://genome.gbf.de/  
and  
\* Max-planck Institute for Molecular Genetics,  
\* Inneustraße 73, D-14195 Berlin, Germany,  
\* e.mail: info-chr21@molgen.mpg.de  
\* URL: http://chr21.rz-berlin.mpg.de/.  
Location/Qualifiers  
1. 340000  
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/note="Accession No. AF064857"  
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2398..2495  
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/rpt\_family="Simple\_repeat"  
/rpt\_type=TANDEM  
complement(2496..2878)  
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2879..2931  
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repeat\_region

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/rpt_type=TANDEM
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/rpt_family="SINE/Alu"
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complement(6887..7067)
/note="L1MD3"
/rpt_family="LINE/L1"
/rpt_type=DISPERSED
complement(8482..8762)
/note="AluJo"
/rpt_family="SINE/Alu"
/rpt_type=DISPERSED
complement(8865..8964)
/note="L2"
/rpt_family="LINE/L2"
/rpt_type=DISPERSED
9131..9424
/note="AluSq"
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complement(9989..10077)
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/rpt_type=TANDEM
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          /number=5
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Best Local Similarity 100.0%; Pred. No. 1.7e-166;
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 368 AGTTATGGGAGAGCTGTTTCATCCAGTGTAACTTTAGTCGCTGAGATGAACCTTG 427
Db 273834 AGTTATGGGAGAGCTGTTTCATCCAGTGTAACTTTAGTCGCTGAGATGAACCTTG 273893

QY 428 TGAAGTTACTTGTCTACCTCCACACTGGACCCGGCTCCCGGATATTTCTCGGAGCTCGG 487
Db 273894 TGAAGTTACTTGTCTACCTCCACACTGGACCCGGCTCCCGGATATTTCTCGGAGCTCGG 273953

QY 488 TCTCTGTGTAGCATTCAAGCTATTATTTTGTTCGGGAGCCGACGACCTTCAAAGTGC 547
Db 273954 TCTCTGTGTAGCATTCAAGCTATTATTTTGTTCGGGAGCCGACGACCTTCAAAGTGC 274013

QY 548 AGTGAGCATCTGGCTCTGACCCACAGAGCAATGGGACTTTTGACTTGCCTGGCTACCTG 607
Db 274014 AGTGAGCATCTGGCTCTGACCCACAGAGCAATGGGACTTTTGACTTGCCTGGCTACCTG 274073

QY 608 GAAGAGCTGAAGGCCCGCAAGTCTGCAACTGTAAATCTCACTGTGATTGGTGTCCCCA 667
Db 274074 GAAGAGCTGAAGGCCCGCAAGTCTGCAACTGTAAATCTCACTGTGATTGGTGTCCCCA 274133

QY 668 AG 669
Db 274134 AG 274135

RESULT 9
CH179K04      182532 bp      DNA      linear      PRI 16-OCT-2003
LOCUS      Pan troglodytes chromosome 22 BAC CH251-179K04, complete sequence.
DEFINITION      AL954228
ACCESSION      AL954228.1 GI:37619870
VERSION      HTG.
KEYWORDS      Pan troglodytes (chimpanzee)
SOURCE      Pan troglodytes
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE      1 (bases 1 to 182532)
AUTHORS      The Chimpanzee Chromosome 22 Sequencing Consortium
CONSTRM      Chimpanzee chromosome 22 genomic sequence
TITLE      Unpublished
JOURNAL
REFERENCE      2 (bases 1 to 182532)
AUTHORS      Scharfe, M., Berg, C., Conrad, A., Hornischer, K., Loehnert, T.H.,
      Ludewig, M., Thies, S., Weber, K. and Bloeker, H.
DIRECT SUBMISSION
TITLE      Submitted (03-JUN-2003) GBF, Dept. of Genome Analysis, Mascheroder
      Weg 1, D-38124 Braunschweig, Germany, E-mail: info.genome@gbf.de
JOURNAL      The Chimpanzee Chromosome 22 Sequencing Consortium consists of :
      Shanghai, China
      Taiwan;
      ----- Genome Center
      Center: GBF, Braunschweig
      Center code: GBF
      Web site: http://genome.gbf.de/
      Contact: info.genome@gbf.de
      ----- Project information
      Center project name:
      Center clone name: CH251-179K04
      ----- Summary Statistics
      Sequencing vector: ###;

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Chemistry: Dye-terminator-amersham: ## of reads
Chemistry: Dye-primer-amersham: ## of reads
Assembly program: ##
Consensus quality: 0 bases at least Q40
Consensus quality: 0 bases at least Q30
Consensus quality: 0 bases at least Q20
Estimated insert size: #: agarose-fp estimation
Estimated insert size: 182532; sum-of-contigs estimation
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PROGRAMS AND PARAMETERS USED FOR ANNOTATION:
+*****+
+ Analysis and annotation were performed with the automatic +
+ 'first-pass' annotation and submission tool +
+ 'AnnoMitter' (Hornischer & Bloeker). +
+ Programs used by 'AnnoMitter': +
+*****+
Location/Qualifiers
1. 182532
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/db_xref="taxon:9598"
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1. 182532
/note="assembly fragment-clone end:T7-vector side:left
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Best Local Similarity 100.0%; Pred. No. 5.4e-106;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 460 GGCTCCGGATATTTCTGGAGTCGCTCTCTGGTCAGCCATTCAAGCTATTATTTC 519
Db 17884 GGCTCCGGATATTTCTGGAGTCGCTCTCTGGTCAGCCATTCAAGCTATTATTTC 17943

QY 520 TTCGGAGCCAGGACCTTCAAGTCAGTGACATCTCGCTCGCTGACCCACAGAGCA 579
Db 17944 TTCGGAGCCAGGACCTTCAAGTCAGTGACATCTCGCTCGCTGACCCACAGAGCA 18003

QY 580 ATGGGACTTTGACTTGGTGCTACCTGGAAGACCTGGAAGCCCGGAGCTCTCAACTG 639
Db 18004 ATGGGACTTTGACTTGGTGCTACCTGGAAGACCTGGAAGCCCGGAGCTCTCAACTG 18063

QY 640 TAAATCTCACTGTGATTCGG 659
Db 18064 TAAATCTCACTGTGATTCGG 18083

RESULT 10
BS000162 156288 bp DNA linear PRI 07-OCT-2003
LOCUS Pan troglodytes chromosome 22 clone:PTB-060F12, map 22, complete
DEFINITION sequences.
ACCESSION BS000162
VERSION BS000162.1 GI:37537429
KEYWORDS Htg..
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE
1 The Chimpanzee Chromosome 22 Sequencing Consortium.
DNA sequence of chimpanzee chromosome 22 and its evolutionary
implications
Unpublished
JOURNAL
2 (bases 1 to 156288)
AUTHORS Saitou,N., Kim,C., Kitano,T., Oota,S., Shimada,M., Kryukov,K.,
Tomiki,T. and Kohara,Y.
Direct Submission
Submitted (15-MAY-2003) Naruya Saitou, National Institute of
Genetics (NIG), Division of Population Genetics, Illi Yata,
Mishima, Shizuoka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp,

URL:http://sayer.lab.nig.ac.jp/, Tel:81-55-981-6790,
Fax:81-55-981-6789)
The Chimpanzee Chromosome 22 Sequencing Consortium consists of:
*Chinese National Human Genome Center at Shanghai, Shanghai, China;
*GBF, Dept. of Genome Analysis, Braunschweig, Germany; *Institute
of Molecular Biotechnology, Jena, Germany; *KIBB Genome Research
Center, Daejeon, Korea;
*Max-Planck-Institute for Molecular Genetics, Berlin, Germany;
*National Institute of Genetics, Mishima, Japan;
*National Yang Ming University Genome Research Center, Taipei,
Taiwan;
*RIKEN Genomic Sciences Center, Yokohama, Japan.
----- Genome Center
Center: National Institute of Genetics
Center code: NIG
Web site: http://sayer.lab.nig.ac.jp/
Contact: nsaitou@genes.nig.ac.jp
----- Project Information
Center project name: The Chimpanzee Chromosome 22 Sequencing Project
Center clone name: PTB-060F12
----- Summary Statistics
Sequencing vector: pUC118; 100% of reads
Chemistry: Dye-terminator Big Dye and dGTP; 100% of reads Assembly
Program: Phrap; version 0.990329
Consensus quality: 156,231 bases at least Q40
Consensus quality: 156,288 bases at least Q30
Consensus quality: 156,288 bases at least Q20
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This sequence was finished as follows unless otherwise noted: all
regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30);
an attempt was made to resolve all sequencing problems, such as
compressions and repeats; all regions were covered by at one
plasmid
subclone or more than one M13 subclone;
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Source information:
The PTB1 chimpanzee BAC library was prepared from DNA isolated from
cultured cells established from the blood of a single male
chimpanzee.
Clones may be obtained from Asao Fujiyama and co-workers
(http://www.gsc.riken.go.jp).
VECTOR: pKS145
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Sequence Quality Assessment:
This entry has been annotated with sequence
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in
10,000 bp.
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Neighboring clones: CH251-179K04 (left) and PTB-103H04 (right).
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FEATURES
source
Query Match 12.3%; Score 145; DB 9; Length 156288;
Best Local Similarity 100.0%; Pred. No. 2.3e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 GAGTCGCTCTCTGGTCAGCCATTCAAGCTATTATTTCGCGAGCCGACCTT 539
Db 1 GAGTCGCTCTCTGGTCAGCCATTCAAGCTATTATTTCGCGAGCCGACCTT 60

QY 540 CAAGTCGAGTCAGCATCTGCTGCTGACCCACAGCAATGGGACTTTGACTTCGCTG 599

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Db      61 CAAAGTCAGTCAGCATCTGCTGTGACCCACAGAGCAATGGGACTTTTGACTTGCCTG 120
QY      600 GCTACTGGAGAGCCTGAAGGCC 624
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Db      121 GCTACTGGAGAGCCTGAAGGCC 145
      |||||

RESULT 11
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DEFINITION Homo sapiens BAC derived from chromosome 21q22.3, complete
sequence, containing PEP19 (PCP4) gene.
ACCESSION AF064857
VERSION   AF064857.1 GI:3171149
KEYWORDS HTG.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 199665)
          Taudien,S., Nordiek,G., Korenberg,J., Drescher,B., Weber,J.,
          Schatnevoy,R. and Rosenthal,A.
          Submitted (11-MAY-1998) Genome Analysis, Institute for Molecular
          Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
FEATURES
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QY 255 GCGAATTCACCTCGAGATGATCATCCAAATGTGGAGCCGAGTCGATTCGGGGAAACATC 314  
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Db 191622 GCGAATTCACCTCGAGATGATCATCCAAATGTGGAGCCGAGTCGATTCGGGGAAACATC 191681  
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QY 315 AGATGACGAGCTC 326

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RESULT 13  
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LOCUS Homo sapiens chromosome 21q22.3 cosmid Q11M15, complete sequence.  
DEFINITION AF045450  
ACCESSION AF045450  
VERSION AF045450.1 GI:2895783  
KEYWORDS HTG.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 40205)  
AUTHORS Taudien,S. and Rosenthal,A.  
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 40205)  
AUTHORS Taudien,S., Nordieck,G., Dagand,E., Hildmann,T., Drescher,B.,  
Weber,J., Rosenthal,A. and Yaspo,M.L.  
JOURNAL Direct Submission

TITLE Submitted (29-JAN-1998) Genome Analysis, Institut for Molecular  
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany

FEATURES Location/Qualifiers

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DB 14773 CTGTCTGCCATCTCAATAACAAGAGATGGGCTTGTGATTTTCTCCACGGT 14825  
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DEFINITION sequence.  
ACCESSION AF064860  
VERSION AF064860.2 GI:18958624  
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ORGANISM Homo sapiens  
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REFERENCE 1 (bases 1 to 170121)  
AUTHORS Hattori, M., Fujiwara, A., Taylor, T.D., Watanabe, H., Yada, T.,  
Park, H.-S., Toyoda, A., Ishii, K., Totoki, Y., Choi, D.-K., Soeda, E.,  
Ohki, M., Takagi, T., Sakaki, Y., Taudien, S., Blechschmidt, K.,  
Polley, A., Menzel, D., Delabar, J., Kumpf, K., Lehmann, R.,  
Patterson, D., Reichwald, K., Rump, A., Schillhabel, M.B., Schudy, A.,  
Zimmermann, W., Rosenthal, A., Kudoh, J., Kawasaki, K., Asakawa, S.,  
Shintani, A., Sasaki, T., Nagamine, K., Mitsuoka, S.,  
Antonarakis, S.E., Minoshima, S., Shimizu, N., Nordsiek, G.,  
Hornischer, K., Brandt, P., Scharfe, M., Schoen, O., Desario, A.,  
Reichelt, J., Kauer, G., Bloeker, H., Ramser, J., Beck, A., Klages, S.,  
Hennig, S., Riessmann, L., Dagand, E., Haaf, T., Wehrmeyer, S.,  
Borzym, K., Gardiner, K., Nizetic, D., Francis, F., Lehrach, H.,  
Reinhardt, R. and Yaspo, M. Laure.  
TITLE The DNA sequence of human chromosome 21  
JOURNAL Nature 405 (6784), 311-319 (2000)  
MEDLINE 20289799  
PUBMED 10830953  
REFERENCE 2 (bases 1 to 170121)  
AUTHORS Rump, A., Dagand, E., Hildmann, T., Nordsiek, G., Drescher, B.,  
Weber, J., Schattevoy, R., Yaspo, M.-L. and Rosenthal, A.  
TITLE Direct Submission  
JOURNAL Submitted (12-MAY-1998) Genome Analysis, Institute of Molecular  
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany  
REFERENCE 3 (bases 1 to 170121)  
AUTHORS Rump, A., Dagand, E., Hildmann, T., Nordsiek, G., Drescher, B.,  
Weber, J., Schattevoy, R., Yaspo, M.-L., Rosenthal, A., Yaspo, M.-L. and  
Rosenthal, A.  
TITLE Direct Submission  
JOURNAL Submitted (27-FEB-2002) Genome Analysis, Institute of Molecular  
Biotechnology, Beutenbergstr. 11, Jena 07745, Germany  
REFERENCE 4 (bases 1 to 170121)  
AUTHORS Rump, A., Dagand, E., Hildmann, T., Nordsiek, G., Drescher, B.,  
Weber, J., Schattevoy, R., Yaspo, M.-L. and Rosenthal, A.  
TITLE Direct Submission  
JOURNAL Submitted (05-MAR-2002) Genome Analysis, Institute of Molecular  
Biotechnology, Beutenbergstr. 11, Jena 07745, Germany  
COMMENT On Feb 27, 2002 this sequence version replaced gi:171153.  
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VERSION AB090820.1 GI:28569877  
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1 Kojima, K.K. and Fujiwara, H.  
Evolution of Target Specificity in R1 Clade Non-LTR Retrotransposons  
Mol. Biol. Evol. 20 (3), 351-361 (2003)  
12644555  
2 (bases 1 to 6470)  
Kojima, K.K. and Fujiwara, H.  
Direct Submission  
Submitted (26-AUG-2002) Kenji K Kojima, University of Tokyo, Department of Integrated Biosciences, Graduate School of Frontier Sciences; Bioscience Building 501, 5-1-5 Kashiwanoha, Kashiwa, Chiba 277-8562, Japan [E-mail:kk27513@mail.ecc.u-tokyo.ac.jp, Tel:81-4-7136-3661, Fax:81-4-7136-3660]  
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ORIGIN

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QY 847 GCTGCTGCCGTGTGTTGTTTCTGCTG 871  
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Db 1574 GCTGCTGCCGTGTGTTGTTTCTGCTG 1550  
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Job time : 4833.88 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: September 14, 2004, 19:19:38 ; Search time 504.04 Seconds  
(without alignments)  
9903.249 Million cell updates/sec

Title: US-09-729-264-1  
Perfect score: 1175  
Sequence: 1 ctgtctgccatctgaataa.....Gtaatacaactgtagtatag 1175

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0  
Searched: 3373863 seqs, 2124099041 residues  
Word size : 0  
Total number of hits satisfying chosen parameters: 5744508

Minimum DB seq length: 16  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N Geneseq 29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1175	100.0	1175	6	ABK13028 DNA encod
2	1076	91.6	2051	9	ADB62950 Human cDN
3	1074	91.4	1240	6	ABK13030 DNA encod
4	1027	87.4	1168	6	ABK13029 DNA encod
5	739	62.9	1139	6	ABK13031 DNA encod
6	728	62.0	1392	5	AAS92356 DNA encod
7	217	18.5	474	8	ACH16130 Human adu
8	144	12.3	401	4	AAI36582 Probe #52
9	25	2.1	357	5	Aai04335 Probe #43
10	24	2.0	6507	4	ABK15493 Drosophil
11	24	2.0	59967	4	ABL15492 Drosophil
12	23	2.0	1195	6	ABK13032 DNA encod
13	22	1.9	141	2	AAV99339 5' PCR pr
14	22	1.9	767	6	ABN99162 Arabidops
15	22	1.9	1200	2	AAV35364 Human GDN
16	22	1.9	1200	2	AAV35365 Human GDN
17	22	1.9	1203	3	AAAI2547 DNA encod
18	22	1.9	1699	2	AAV00251 Human Ret
19	22	1.9	1792	3	AAZ29104 Human GPR
20	22	1.9	1809	2	AAV99333 Glial cel
21	22	1.9	1829	3	Aaz93702 PRO538 DN
22	22	1.9	1829	3	AAH8519 Human PRO
23	22	1.9	1829	3	AAH7617 Human PRO

24	22	1.9	1829	3	AAH54101 PRO538 cD
25	22	1.9	1829	3	AAC58234 Human PRO
26	22	1.9	1837	3	Aaz29105 Human GPR
27	22	1.9	1837	3	AAH8520 Human PRO
28	22	1.9	1837	3	AAC58235 Human PRO
29	22	1.9	1878	2	AAV99334 Glial cel
30	22	1.9	1991	2	AAV99329 cDNA enco
31	22	1.9	3942	2	AAV35851 Rat angio
32	22	1.9	4142	7	ABT41796 Toxicity
33	22	1.9	4142	9	ADB52524 Primary r
34	21	1.8	269	3	AAC10184 Human sec
35	21	1.8	493	8	ACH23839 Human adu
36	21	1.8	550	5	AAS05528 Mammalian
37	21	1.8	921	5	AAS80140 DNA encod
38	21	1.8	1126	6	ABQ61025 Human dif
39	21	1.8	1558	5	AAH81511 Human pol
40	21	1.8	1679	4	AAI93530 Human pol
41	21	1.8	1830	5	AAS80204 DNA encod
42	21	1.8	2649	5	AAS88493 Drosophil
43	21	1.8	2803	4	ABL10241 Drosophil
44	21	1.8	7782	4	ABL20110 Drosophil
45	21	1.8	8747	4	ABL10240 Drosophil

ALIGNMENTS

RESULT 1  
ID ABK13028 standard; cDNA; 1175 BP.  
XX  
AC ABK13028;  
XX  
DT 23-APR-2002 (first entry)  
XX  
DE DNA encoding human B7-like protein, B7-L\_h1.  
XX  
KW Human; B7-like protein; B7-L; antiinfertility; gynaecological;  
KW antitumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic;  
KW antiinflammatory; dermatological; antipsoriatic; neuroprotective;  
KW antidiabetic; haemostatic; antithyroid; antitumor; antiallergic;  
KW antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer;  
KW reproductive disorder; graft versus host disease; autoimmune disease;  
KW toxic shock syndrome; allergy; nephropathy; skin disorder;  
KW endocrinopathy; lymphoproliferative disorder; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 27..1175  
FT /\*tag= a  
FT /product= "B7-like protein, B7-L\_h1"  
XX  
WO200200710-A2.  
XX  
03-JAN-2002.  
XX  
28-JUN-2001; 2001WO-US020719.  
XX  
28-JUN-2000; 2000US-0214512P.  
XX  
28-NOV-2000; 2000US-00729264.  
XX  
(AMGE-) AMGEN INC.  
XX  
Welcher AA, Sarmiento UM, Schultz HJ, Chute HT;  
XX  
WPI; 2002-130881/17.  
XX  
P-PSDB; AAU75540.  
XX  
New B7-like polypeptides, polynucleotides and their modulators, useful  
XX for diagnosing, preventing and treating reproductive, immune and  
XX proliferative disorders, e.g. cancer and arteriosclerosis.  
XX

PS	Claim 1; Fig 1; 135pp; English.	
XX	The invention relates to an isolated B7-like (B7-L) polypeptide (I). The	
CC	polypeptide, polynucleotide encoding it and antibody against (I) are	
CC	useful for treating B7-like polypeptide-related disease, disorders or	
CC	conditions including reproductive disorders (e.g. infertility,	
CC	miscarriage, preterm labour and delivery and endometriosis) and	
CC	proliferative disorders. Antibodies, soluble proteins comprising	
CC	extracellular domains and other regulators of B7-L polypeptides are	
CC	useful for enhancing the immune response to tumours. (I) plays a role in	
CC	growth and maintenance of cancer cells based on the observation of	
CC	seminal vesicle hyperplasia in transgenic mice overexpressing B7-L	
CC	polypeptide. Hence modulators of (I) are useful for the treatment of	
CC	cancer including seminal vesicle cancer, lung, brain, breast, ovarian,	
CC	testicular cancer and cancers of haematopoietic system. B7-L polypeptide	
CC	pathway can be manipulated to regulate cytotoxic T-lymphocyte response in	
CC	allograft transplantation, graft versus host disease, T-cell dependent B-	
CC	cell mediated diseases and autoimmune diseases. B7-L molecules are useful	
CC	for alleviating the symptoms associated with diseases involving chronic	
CC	immune cell dysfunction or to treat autoimmune diseases such as systemic	
CC	lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes,	
CC	immune thrombocytopenic purpura and psoriasis, chronic inflammatory	
CC	disease such as inflammatory bowel disease (Crohn's disease and	
CC	ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and	
CC	diabetes mellitus. They are also useful as immunosuppressive agents for	
CC	bone marrow and organ transplantation or to prolong graft survival. B7-L	
CC	molecules are also useful for diagnosis and treatment of diseases	
CC	involving abnormal cell proliferation, including arteriosclerosis and	
CC	vascular restenosis. Antagonists of B7-L polypeptides are useful for	
CC	alleviation of toxic shock syndrome or allensensitisation due to blood	
CC	transfusions, and for treatment of allergy, asthma and hypersensitivity	
CC	reactions, nephropathies (e.g. glomerulonephritis), skin disorders	
CC	(pemphigus and pemphigoid), endocrinopathies (Grave's disease), various	
CC	pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease,	
CC	anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia	
CC	gravis, and lymphoproliferative disorders such as multiple myeloma. The	
CC	present sequence represents the coding sequence of human B7-L <sub>h1</sub>	
XX		
SQ	Sequence 1175 BP; 295 A; 307 C; 286 G; 287 T; 0 U; 0 Other;	
	Query Match 100.0%; Score 1175; DB 6; Length 1175;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 1175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CTGTCTGCCATCGAATAACAGAGATGGGGCTTGATTTCTCCACGGTCTCGGT 60	
DB	1 CTGTCTGCCATCGAATAACAGAGATGGGGCTTGATTTCTCCACGGTCTCGGT 60	
QY	61 CTGTAATGAGTCTAGAGCCCGCCAGATGCAACAGTCTGAAGGGCTCCAGGCTC 120	
DB	61 CTGTAATGAGTCTAGAGCCCGCCAGATGCAACAGTCTGAAGGGCTCCAGGCTC 120	
QY	121 GCTTCAATGCAACCGTCTCCAGGGCTGGAAGCTCATCATGTTGGCTCTCAGTGCATGG 180	
DB	121 GCTTCAATGCAACCGTCTCCAGGGCTGGAAGCTCATCATGTTGGCTCTCAGTGCATGG 180	
QY	181 TGGTCTAAGCGTCAAGCGCTCAGATGAGCCCATGACCAATGACCGCTTCACTCTCAGA 240	
DB	181 TGGTCTAAGCGTCAAGCGCTCAGATGAGCCCATGACCAATGACCGCTTCACTCTCAGA 240	
QY	241 GGTACGACAGGGCGGGAATTCACCTCGAGATGATCATCACAATGTGGAGCCAGTG 300	
DB	241 GGTACGACAGGGCGGGAATTCACCTCGAGATGATCATCACAATGTGGAGCCAGTG 300	
QY	301 ATTCTGGGGAACATCAGATGAGCTCCAGAACAGTGGCTGATGATGATCTGCTTACCTTA 360	
DB	301 ATTCTGGGGAACATCAGATGAGCTCCAGAACAGTGGCTGATGATGATCTGCTTACCTTA 360	
QY	361 CGGTCAAGTTATGGAGAGCTGTTTCAATCCAGTGTAAATCTTGTAGTCGTGGAATG 420	
DB	361 CGGTCAAGTTATGGAGAGCTGTTTCAATCCAGTGTAAATCTTGTAGTCGTGGAATG 420	
QY	421 AACTTTGTGAAGTTACTTGTCTACCTCACACTGGACCGGCTCCCGGATATTTCTGGG 480	

DB	421 AACTTTGTGAAGTTACTTGTCTACCTCACACTGGACCGGCTCCCGGATATTTCTGGG 480	
QY	481 AGCTCGGTCTCTGTCAGCCATTAAGCTATTATTTCTTCGGAGCCAGGACCTTC 540	
DB	481 AGCTCGGTCTCTGTCAGCCATTAAGCTATTATTTCTTCGGAGCCAGGACCTTC 540	
QY	541 AAAGTGCAGTGCAGTCTCTGGCTCTGACCCCAAGCAATGGGATTTGACCTTGGGTG 600	
DB	541 AAAGTGCAGTGCAGTCTCTGGCTCTGACCCCAAGCAATGGGATTTGACCTTGGGTG 600	
QY	601 CTACTTGAAGAGCTTGAAGGCCGCAAGTCTGCAACTGTAATCTCACTGTGATTCGGT 660	
DB	601 CTACTTGAAGAGCTTGAAGGCCGCAAGTCTGCAACTGTAATCTCACTGTGATTCGGT 660	
QY	661 GTCCCCAAGACACTGAGGTGGTATTAAATATCCAGGTGTATTATCAAGTTTACCGAGTT 720	
DB	661 GTCCCCAAGACACTGAGGTGGTATTAAATATCCAGGTGTATTATCAAGTTTACCGAGTT 720	
QY	721 TAGGTTTTCATTGCTCTACTTTGGGCAAGTGGACTTGGAGTAGCAGGACCATGCTTC 780	
DB	721 TAGGTTTTCATTGCTCTACTTTGGGCAAGTGGACTTGGAGTAGCAGGACCATGCTTC 780	
QY	781 TGACGGCGAGCTGACTTACTTACAAATAGCTGCTGCTGCCGCCGCTGTTGTGTGGCT 840	
DB	781 TGACGGCGAGCTGACTTACTTACAAATAGCTGCTGCTGCCGCCGCTGTTGTGTGGCT 840	
QY	841 GCAACTGCTCTGCGGTGTTGTTTCTGCTGTAGAGAAAAGAGGATTTCTGATTCAAT 900	
DB	841 GCAACTGCTCTGCGGTGTTGTTTCTGCTGTAGAGAAAAGAGGATTTCTGATTCAAT 900	
QY	901 TTCAAAAAGAAATCTGAAAAAGAGAGCAACAAAGAAACTGAGACAGAAAGTGAATG 960	
DB	901 TTCAAAAAGAAATCTGAAAAAGAGAGCAACAAAGAAACTGAGACAGAAAGTGAATG 960	
QY	961 AAAACTCGGCTACAATTCAGATCAACAAAGAGCCAGACACCGCTTCTCTCCCTCCCA 1020	
DB	961 AAAACTCGGCTACAATTCAGATCAACAAAGAGCCAGACACCGCTTCTCTCCCTCCCA 1020	
QY	1021 AATCCTGTGAATCCAGTGAATCTCTGAACAAAGAAACAGTAGCTGTGGCCCTCTCACCAGC 1080	
DB	1021 AATCCTGTGAATCCAGTGAATCTCTGAACAAAGAAACAGTAGCTGTGGCCCTCTCACCAGC 1080	
QY	1081 GGGCTGATCAACGTCCACCCAGGCGAGCAAGTATCCACAGGCTTCTTTTAACTGGCCA 1140	
DB	1081 GGGCTGATCAACGTCCACCCAGGCGAGCAAGTATCCACAGGCTTCTTTTAACTGGCCA 1140	
QY	1141 GTCTGTGAAGGTCAAGTAAATACAACTGTAGTATAG 1175	
DB	1141 GTCTGTGAAGGTCAAGTAAATACAACTGTAGTATAG 1175	
RESULT 2		
ADB62950	ADB62950 standard; cDNA; 2051 BP.	
ID	ADB62950 standard; cDNA; 2051 BP.	
XX		
AC	ADB62950;	
XX		
DT	04-DEC-2003 (first entry)	
XX		
DE	Human cDNA encoding clone PLACE60177880.	
XX		
KW	Human; ss; gene; pharmaceutical; diagnostic; gene therapy;	
KW	tissue regeneration; cell regeneration; membrane protein;	
KW	signal transduction-related protein; transcription-related protein;	
KW	osteoporosis; neurological disease; cancer; tumour.	
OS	Homo sapiens.	
XX		
Key	Location/Qualifiers	
FT	104..1327	
FT	/tag= a	
FT	/product= "Clone PLACE60177880 protein"	



XX EP1308459-A2.  
XX 07-MAY-2003.  
XX 28-MAR-2002; 2002EP-00007401.  
XX 05-NOV-2001; 2001JP-00379298.  
XX 25-JAN-2002; 2002US-00350978.  
XX (HELI-) HELIX RES INST.  
XX PA (RES-) RES ASSOC BIOTECHNOLOGY.  
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
XX Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
XX WPI: 2003-450961/43.  
XX P-PSDB; ADB64920.  
XX New polynucleotides and polypeptides, useful for developing a diagnostic  
XX marker or medicines for regulation of their expression and activity, or  
XX as targets of gene therapy.  
XX Claim 1; Page; 222pp; English.  
XX The invention discloses a polynucleotide comprising a sequence selected  
XX from 1970 fully defined nucleotide sequences which encode novel  
XX polypeptides. Also claimed is a polypeptide encoded by the polynucleotide  
XX or its partial peptide, an antibody binding to the polypeptide or peptide  
XX of the polynucleotide, immunologically assaying the polypeptide or  
XX peptide of the polynucleotide by contacting the polypeptide or peptide  
XX with the antibody of the encoded protein, and observing the binding  
XX between the two, a transformant carrying the polynucleotide in an  
XX expressible manner and an antisense polynucleotide. The oligonucleotide  
XX is useful as a primer for synthesising the polynucleotide, or as a probe  
XX for detecting the polynucleotide. The polynucleotides and encoded  
XX proteins are useful as pharmaceutical agents and many disease-related  
XX genes may be included in them, for developing a diagnostic marker or  
XX medicines for regulation of their expression and activity, or as targets  
XX of gene therapy. The genes are involved in tissue and/or cell  
XX regeneration. Membrane proteins, signal transduction-related proteins,  
XX encoding them can be used as indicators for diseases (e.g. osteoporosis,  
XX neurological diseases, cancer, tumours). The cDNA may be used to regulate  
XX the activity or expression of the encoded protein to treat diseases. The  
XX sequence presented is a cDNA of the invention. Note: Some of the sequence  
XX data for this patent is not represented in the printed specification, but  
XX is based on sequence information supplied by the European Patent Office.  
XX SQ Sequence 2051 BP; 580 A; 463 C; 474 G; 534 T; 0 U; 0 Other;  
Query Match 91.6%; Score 1076; DB 9; Length 2051;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1126; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 49 ACGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCGCCAGAAATGCAACAGTCTCTGAAGG 108  
DB 201 ACGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCGCCAGAAATGCAACAGTCTCTGAAGG 260  
QY 109 GCTCCAGGCTCGCTTCAACTGACCGTCTCCAGGCTGGAAGCTCATCATGTGGGCTC 168  
DB 261 GCTCCAGGCTCGCTTCAACTGACCGTCTCCAGGCTGGAAGCTCATCATGTGGGCTC 320  
QY 169 TCAGTGACATGGTGGTCTGAAGCGTCAGGCCCATGGGCCCATCATCAATGACCGCT 228  
DB 321 TCAGTGACATGGTGGTCTGAAGCGTCAGGCCCATGGGCCCATCATCAATGACCGCT 380  
QY 229 TCACCTCTCAGAGGTACGACCGAGGGGGAACTTCACTCGGAGATGATCATCCACAATG 298  
DB 381 TCACCTCTCAGAGGTACGACCGAGGGGGAACTTCACTCGGAGATGATCATCCACAATG 440  
QY 289 TGGAGCCGAGTGATTCGGGGAAACATCAGATGACGCTCCAGAACAGTGGCCTGATGGAT 348

RESULT 3

ABK13030

ID ABK13030 standard; cDNA; 1240 BP.

XX ABK13030;

AC  
XX  
XX  
DT 23-APR-2002 (first entry)

XX DNA encoding human B7-like protein, B7-L\_h3.

XX Human; B7-like protein; B7-L; antiinfectility; gynaecological;  
XX antitumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic;  
XX antinflammatory; dermatological; antipsoriatic; neuroprotective;

DB 441 TGGAGCCCGAGTATCGGGGAACATCAGATCGAGCCTCAGAACAGTCCGCTCGCATGGAT 500  
QY 349 CTGCTTACCTTACCGTCCAAAGTTATGGAGAGCTGTTCAATCCCAAGTGTAAATCTTTAG 408  
DB 501 CTGCTTACCTTACCGTCCAAAGTTATGGAGAGCTGTTCAATCCCAAGTGTAAATCTTTAG 560  
QY 409 TCGCTGAGAATGAACCTTGTGAAGTACTTGTCTACCTCAGCTGGACCCGGCTCCCGG 468  
DB 561 TCGCTGAGAATGAACCTTGTGAAGTACTTGTCTACCTCAGCTGGACCCGGCTCCCGG 620  
QY 469 ATATTCTCTGGAGCTCGGTCTCTCTGGTTCAGCCATTCAAGCTATTATTCTTCTCGGAGC 528  
DB 621 ATATTCTCTGGAGCTCGGTCTCTCTGGTTCAGCCATTCAAGCTATTATTCTTCTCGGAGC 680  
QY 529 CCAGGACCTTCAAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 588  
DB 681 CCAGGACCTTCAAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 740  
QY 589 TGACTTGGTGGTCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 648  
DB 741 TGACTTGGTGGTCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 800  
QY 649 CTGTGATTTCGGTGTCCCAAGACACTCGAGGTGCTATTATATATTCAGGTGTATTATCAA 708  
DB 801 CTGTGATTTCGGTGTCCCAAGACACTCGAGGTGCTATTATATTCAGGTGTATTATCAA 860  
QY 709 GTTTACGAGTTAGTGTTCCTTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768  
DB 861 GTTTACGAGTTAGTGTTCCTTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 920  
QY 769 GCACCATGCTTCTGACGCGGACGCTGCTTCAATACGCTGCTGCTGCTGCTGCTGCTGCTG 828  
DB 921 GCACCATGCTTCTGACGCGGACGCTGCTTCAATACGCTGCTGCTGCTGCTGCTGCTGCTG 980  
QY 829 GTTGTCTGGTGTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 888  
DB 981 GTTGTCTGGTGTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1040  
QY 889 TTCGTATTTCATTTTCAAAAGAAATCTGAAAAGAGAGACAAACAAAGAACTGAGACAG 948  
DB 1041 TTCGTATTTCATTTTCAAAAGAAATCTGAAAAGAGAGACAAACAAAGAACTGAGACAG 1100  
QY 949 AAAGTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1008  
DB 1101 AAAGTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 1160  
QY 1009 CTCTCCCTCCCAATCTCTGTAATCCAGTGTCTGTAATCCAGTGTCTGTAATCCAGTGTCTG 1068  
DB 1161 CTCTCCCTCCCAATCTCTGTAATCCAGTGTCTGTAATCCAGTGTCTGTAATCCAGTGTCTG 1220  
QY 1069 CTCTCAGCAGCGGGTGTATCAACGCTCCAGGCGGCGAGCAAGTCAATCCAGGCTTCTT 1128  
DB 1221 CTCTCAGCAGCGGGTGTATCAACGCTCCAGGCGGCGAGCAAGTCAATCCAGGCTTCTT 1280  
QY 1129 TTAATCTGGCCAGTCTCTGGAAGTCTGTAATCAATCAATCAATCAATCAATCAATCAAT 1175  
DB 1281 TTAATCTGGCCAGTCTCTGGAAGTCTGTAATCAATCAATCAATCAATCAATCAATCAAT 1327

antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic;  
antialstematic; nephrotropic; antibacterial; virucide; tumour; cancer;  
reproductive disorder; graft versus host disease; autoimmune disease;  
toxic shock syndrome; allergy; nephropathy; skin disorder;  
endocrinopathy; lymphoproliferative disorder; gene; ss.  
Homo sapiens.  
Key Location/Qualifiers  
CDS 80..1240  
/\*tag= a  
/product= "B7-like protein, B7-L\_h3"  
WO200200710-A2.  
03-JAN-2002.  
28-JUN-2001; 2001WO-US020719.  
28-JUN-2000; 2000US-0214512P.  
28-NOV-2000; 2000US-00729264.  
(AMGE-) AMGEN INC.  
Welcher AA, Sarmiento UM, Schultz HJ, Chute HT;  
WPI; 2002-130881/17.  
P-PSDB; AAU75542.  
New B7-like polypeptides, polynucleotides and their modulators, useful  
for diagnosing, preventing and treating reproductive, immune and  
proliferative disorders, e.g. cancer and arteriosclerosis.  
Claim 1; Fig 3; 135pp; English.  
The invention relates to an isolated B7-like (B7-L) polypeptide (I). The  
polypeptide, polynucleotide encoding it and antibody against (I) are  
useful for treating B7-like polypeptide-related disease, disorders or  
conditions including reproductive disorders (e.g. infertility, and  
miscarriage, preterm labour and delivery and endometriosis) and  
proliferative disorders. Antibodies, soluble proteins comprising  
extracellular domains and other regulators of B7-L polypeptides are  
useful for enhancing the immune response to tumours. (I) plays a role in  
growth and maintenance of cancer cells based on the observation of  
seminal vesicle hyperplasia in transgenic mice overexpressing B7-L  
polypeptide. Hence modulators of (I) are useful for the treatment of  
cancer including seminal vesicle cancer, lung, brain, breast, ovarian,  
testicular cancer and cancers of haematopoietic system. B7-L polypeptide  
pathway can be manipulated to regulate cytotoxic T-lymphocyte response in  
allograft transplantation, graft versus host disease, T-cell dependent B-  
cell mediated diseases and autoimmune diseases. B7-L molecules are useful  
for alleviating the symptoms associated with diseases involving chronic  
immune cell dysfunction or to treat autoimmune diseases such as systemic  
lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes,  
immune thrombocytopenic purpura and psoriasis, chronic inflammatory  
disease such as inflammatory bowel disease (Crohn's disease and  
ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and  
diabetes mellitus. They are also useful as immunosuppressive agents for  
bone marrow and organ transplantation or to prolong graft survival. B7-L  
molecules are also useful for diagnosis and treatment of diseases  
involving abnormal cell proliferation, including arteriosclerosis and  
vascular restenosis. Antagonists of B7-L polypeptides are useful for  
alleviation of toxic shock syndrome or allosensitisation due to blood  
transfusions, and for treatment of allergy, asthma and hypersensitivity  
reactions, nephropathies (e.g. glomerulonephritis), skin disorders  
(pemphigus and pemphigoid), endocrinopathies (Grave's disease), various  
pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease,  
anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia  
gravis, and lymphoproliferative disorders such as multiple myeloma. The  
present sequence represents the coding sequence of human B7-L\_h3  
Sequence 1240 BP; 318 A; 319 C; 305 G; 298 T; 0 U; 0 Other;

Query Match	91.4%;	Score 1074;	DB 6;	Length 1240;	
Best Local Similarity	99.9%;	Pred. No. 0;			
Matches 1124;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	51	GGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAAGAAATGCAACAGTCTCTGAAGGCC	110		
DB	116	GGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAAGAAATGCAACAGTCTCTGAAGGCC	175		
QY	111	TCCAGGCTCGCTTCAACTGCACCGCTCTCCAGGGCTGGAAGCTCATCATGTGGGCTCTC	170		
DB	176	TCCAGGCTCGCTTCAACTGCACCGCTCTCCAGGGCTGGAAGCTCATCATGTGGGCTCTC	235		
QY	171	AGTGACATGGTGGTCTAAGCGCTCAGGCCCATGAGAGCCCATCATCAACAAATGACCGCTTC	230		
DB	236	AGTGACATGGTGGTCTAAGCGCTCAGGCCCATGAGAGCCCATCATCAACAAATGACCGCTTC	295		
QY	231	ACCTCTCAGAGGTACGACACAGGGGGGAACTTTCACCTCGGAGATGATCATCCACAATGTG	290		
DB	296	ACCTCTCAGAGGTACGACACAGGGGGGAACTTTCACCTCGGAGATGATCATCCACAATGTG	355		
QY	291	GAGCCAGTGATTCGGGGAAACATCAGATGCAGCTCCAGAACAGTCCGCTGATGATCT	350		
DB	356	GAGCCAGTGATTCGGGGAAACATCAGATGCAGCTCCAGAACAGTCCGCTGATGATCT	415		
QY	351	GCTTACCTTACCGTCCAAAGTTATGGGAGAGCTGTTCAATCCCAAGTGTAACTTTGTAGTC	410		
DB	416	GCTTACCTTACCGTCCAAAGTTATGGGAGAGCTGTTCAATCCCAAGTGTAACTTTGTAGTC	475		
QY	411	GCTGAGAAAGCACTTGTGAAGTTACTTGTCTACCTTCACACTGGACCCGGCTCCCGGAT	470		
DB	476	GCTGAGAAAGCACTTGTGAAGTTACTTGTCTACCTTCACACTGGACCCGGCTCCCGAT	535		
QY	471	ATTTCTCTGGAGCTCGGTCTCTCGGTGAGCCATTCAGAGCTATTATTTTGTTCGGAGCCC	530		
DB	536	ATTTCTCTGGAGCTCGGTCTCTCGGTGAGCCATTCAGAGCTATTATTTTGTTCGGAGCCC	595		
QY	531	AGCGACCTTCAAGTGAGTGAGCATCTCGCTCTGACCCACAGACAAATGGGACTTTG	590		
DB	596	AGCGACCTTCAAGTGAGTGAGCATCTCGGTCTGACCCCAAGAGCAATGGGACTTTG	655		
QY	591	ACTTGGTGGCTACTCTGGAAGAGCCCTGAAGGCCCGCAAGTCTGCAACTGTAAATCTCACT	650		
DB	656	ACTTGGTGGCTACTCTGGAAGAGCCCTGAAGGCCCGCAAGTCTGCAACTGTAAATCTCACT	715		
QY	651	GTGATTCGGTGTCTCCCAAGACACTGAGGTGGTATTAAATATTCAGGTGTATTATCAAGT	710		
DB	716	GTGATTCGGTGTCTCCCAAGACACTGAGGTGGTATTAAATATTCAGGTGTATTATCAAGT	775		
QY	711	TTACCGAGTTAGTGTCTTTCCTCTACTTGGGGCAAGTTGGACTTGGACTAGCAGGC	770		
DB	776	TTACCGAGTTAGTGTCTTTCCTCTACTTGGGGCAAGTTGGACTTGGACTAGCAGGC	835		
QY	771	ACCATGCTCTGACGCGCAGCTGACTTCTTACAATACGCTGCTGCTGCGCCGCTCGT	830		
DB	836	ACCATGCTCTGACGCGCAGCTGACTTCTTACAATACGCTGCTGCTGCGCCGCTCGT	895		
QY	831	TGTTGTGGCTGCAAACTGCTGCTGCGGTTGTTGTTCTGCTGTAGAGAAAAGAGGATTT	890		
DB	896	TGTTGTGGCTGCAAACTGCTGCTGCGGTTGTTGTTCTGCTGTAGAGAAAAGAGGATTT	955		
QY	891	CGTATTCAATTTCAAAGAAATCTGMAAAGAGAGAGCAACAAGAACTGAGACAGAA	950		
DB	956	CGTATTCAATTTCAAAGAAATCTGMAAAGAGAGAGCAACAAGAACTGAGACAGAA	1015		
QY	951	AGTGAATGAAACTCCGGCTCAATTCAGATGAACAAAAGAGACACAGACACCGCTTCT	1010		
DB	1016	AGTGAATGAAACTCCGGCTCAATTCAGATGAACAAAAGAGACACAGACACCGCTTCT	1075		
QY	1011	CTCCCTCCCAATCTCTGTAATCCAGTGAATCCTTGAAACAAAGAAACAGTAGCTGGCCCT	1070		
DB	1076	CTCCCTCCCAATCTCTGTAATCCAGTGAATCCTTGAAACAAAGAAACAGTAGCTGGCCCT	1135		
QY	1071	CCTCACAGCGGGCTGATCAACGTCCACCCAGGCCAGCAAGTCAATCCACAGGCTTCTTTT	1130		

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Db      1136 CCTCACCAGGGGCTGATCAAGCTCCACCAGCCAGCAAGTCATCCACAGGCTTCTTTT 1195
QY      1131 AATCTGCCAGCTCTCAGAGGTCAGTAATAACAACCTGTAGTATAG 1175
Db      1196 AATCTGCCAGCTCTCAGAGGTCAGTAATAACAACCTGTAGTATAG 1240

RESULT 4
ABK13029
ID      ABK13029 standard; cDNA; 1168 BP.
AC      ABK13029;
XX
DT      23-APR-2002 (first entry)
DE
DE      DNA encoding human B7-like protein, B7-L_h2.
XX
KW      Human; B7-like protein; B7-L; antiinfertility; gynaecological;
KW      antitumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic;
KW      antiinflammatory; dermatological; antipsoriatic; neuroprotective;
KW      antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic;
KW      antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer;
KW      reproductive disorder; graft versus host disease; autoimmune disease;
KW      toxic shock syndrome; allergy; nephropathy; skin disorder;
KW      endocrinopathy; lymphoproliferative disorder; gene; ss.
XX
OS      Homo sapiens.
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XX      Key      Location/Qualifiers
XX      CDS      8..1168
XX              /*tag= a
XX              /product= "B7-like protein, B7-L_h2"
XX
XX      WO200200710-A2.
XX
XX      03-JAN-2002.
XX
XX      28-JUN-2001; 2001WO-US020719.
XX
XX      28-JUN-2000; 2000US-0214512P.
XX      28-NOV-2000; 2000US-00729264.
XX
XX      (AMGE-) AMGEN INC.
XX
XX      Welcher AA, Sarmiento UM, Schultz HJ, Chute HT;
XX      WPI; 2002-130881/17.
XX      P-PSDB; AAU75541.
XX
XX      New B7-like polypeptides, polynucleotides and their modulators, useful
XX      for diagnosing, preventing and treating reproductive, immune and
XX      proliferative disorders, e.g. cancer and arteriosclerosis.
XX
XX      Claim 1; Fig 2; 135pp; English.
XX
XX      The invention relates to an isolated B7-like (B7-L) polypeptide (I). The
XX      polypeptide, polynucleotide encoding it and antibody against (I) are
XX      useful for treating B7-like polypeptide-related disease, disorders or
XX      conditions including reproductive disorders (e.g. infertility,
XX      miscarriage, preterm labour and delivery and endometriosis) and
XX      proliferative disorders. Antibodies, soluble proteins comprising
XX      extracellular domains and other regulators of B7-L polypeptides are
XX      useful for enhancing the immune response to tumours. (I) plays a role in
XX      growth and maintenance of cancer cells based on the observation of
XX      seminal vesicle hyperplasia in transgenic mice overexpressing B7-L
XX      polypeptide. Hence modulators of (I) are useful for the treatment of
XX      cancer including seminal vesicle cancer, lung, brain, breast, ovarian,
XX      testicular cancer and cancers of haematopoietic system. B7-L polypeptide
XX      pathway can be manipulated to regulate cytotoxic T-lymphocyte response in
XX      allograft transplantation, graft versus host disease, T-cell dependent B-
XX      cell mediated diseases and autoimmune diseases. B7-L molecules are useful
XX      for alleviating the symptoms associated with diseases involving chronic

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CC      immune cell dysfunction or to treat autoimmune diseases such as systemic
CC      lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes,
CC      immune thrombocytopenic purpura and psoriasis, chronic inflammatory
CC      disease such as inflammatory bowel disease (Crohn's disease and
CC      ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and
CC      diabetes mellitus. They are also useful as immunosuppressive agents for
CC      bone marrow and organ transplantation or to prolong graft survival. B7-L
CC      molecules are also useful for diagnosis and treatment of diseases
CC      involving abnormal cell proliferation, including arteriosclerosis and
CC      vascular restenosis. Antagonists of B7-L polypeptides are useful for
CC      alleviation of toxic shock syndrome or allosensitisation due to blood
CC      transfusions, and for treatment of allergy, asthma and hypersensitivity
CC      reactions, nephropathies (e.g. glomerulonephritis), skin disorders
CC      (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various
CC      pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease,
CC      anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia,
CC      gravis, and lymphoproliferative disorders such as multiple myeloma. The
CC      present sequence represents the coding sequence of human B7-L_h2
XX
XX      Sequence 1168 BP; 299 A; 302 C; 288 G; 279 T; 0 U; 0 Other;
SQ

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Query Match      87.4%; Score 1027; DB 6; Length 1168;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1077; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      98 AGTCCTGAGGGCTCCAGGCTCGCTTCAACGTGACCGTCTCCAGGGCTGGAAGCTCAT 157
Db      91 AGTCCTGAGGGCTCCAGGCTCGCTTCAACGTGACCGTCTCCAGGGCTGGAAGCTCAT 150
QY      158 CATGTGGGCTCTCAGTGACATGGTGTCTAAGCGTCAGGCGCCATGGAGCCCATCATCAC 217
Db      151 CATGTGGGCTCTCAGTGACATGGTGTCTAAGCGTCAGGCGCCATGGAGCCCATCATCAC 210
QY      218 CAATGACCGCTTCACTCTCAGAGGTACGACACAGGGCGGGAACCTCACTCGGAGATCAT 277
Db      211 CAATGACCGCTTCACTCTCAGAGGTACGACACAGGGCGGGAACCTCACTCGGAGATCAT 270
QY      278 CATCCACAATGTGAGGCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCG 337
Db      271 CATCCACAATGTGAGGCCAGTGATTCGGGGAACATCAGATGCAGCCTCCAGAACAGTCG 330
QY      338 CCTGCATGGATCTGCTTACCTTACCGTCCAGTTATGGAGAGCTGTTTCATCCAGTGT 397
Db      331 CCTGCATGGATCTGCTTACCTTACCGTCCAGTTATGGAGAGCTGTTTCATCCAGTGT 390
QY      398 TAATCTTTGTAGTCGTCAGAAATGAACCTTGTGAAGTTACTTGTACCTCACACTGGAC 457
Db      391 TAATCTTTGTAGTCGTCAGAAATGAACCTTGTGAAGTTACTTGTACCTCACACTGGAC 450
QY      458 CCGGCTCCCGGATATTTCTTGGGAGCTCGGTCTCTCGTCAGCCATTCAAGCTATTATTT 517
Db      451 CTGGCTCCCGGATATTTCTTGGGAGCTCGGTCTCTCGTCAGCCATTCAAGCTATTATTT 510
QY      518 TGTTCGGAGCCAGCGACCTTCAAAAGTCAGTGAGCATCTGGCTCTGACCCACAGAG 577
Db      511 TGTTCGGAGCCAGCGACCTTCAAAAGTCAGTGAGCATCTGGCTCTGACCCACAGAG 570
QY      578 CAATGGGACTTTGACTTGGCTGGCTACCTGGAAGAGCCTGAAGCCCGCAAGTCTGCAAC 637
Db      571 CAATGGGACTTTGACTTGGCTGGCTACCTGGAAGAGCCTGAAGCCCGCAAGTCTGCAAC 630
QY      638 TGTAAATCTCACTGTGATTCGGTGTCCCAAGACACATGGAGGTGGTATTAAATATCCAGG 697
Db      631 TGTAAATCTCACTGTGATTCGGTGTCCCAAGACACATGGAGGTGGTATTAAATATCCAGG 690
QY      698 TGTATTATCAAGTTTACCAGTTTAGTGTTCCTTTCCTTACCTTGGGGCAAGTTGAGACT 757
Db      691 TGTATTATCAAGTTTACCAGTTTAGTGTTCCTTTCCTTACCTTGGGGCAAGTTGAGACT 750
QY      758 TGGACTAGCAGGCACCATGCTTCTGACGCGGACGTGTACTTCTTACAAATACGCTGCTG 817
Db      751 TGGACTAGCAGGCACCATGCTTCTGACGCGGACGTGTACTTCTTACAAATACGCTGCTG 810

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QY 818 CTGCGCGCGTCTGTTGTTGCTGCAACTGCTGCTGCGCTGTTGTTTCTGCTGTAGAG 877  
Db |||||||  
QY 811 CTGCGCGCGTCTGTTGTTGCTGCAACTGCTGCTGCGCTGTTGTTTCTGCTGTAGAG 870  
Db |||||||  
QY 878 AAAAGAGGATTCGTATTCAATTTCAAAGAAATCTGAAAAGAGAAACAAAGA 937  
Db |||||||  
QY 871 AAAAGAGGATTCGTATTCAATTTCAAAGAAATCTGAAAAGAGAAACAAAGA 930  
Db |||||||  
QY 938 AACTGAGACAGAAAGTGGAAATGAATACTCGGCTGACATTCAGATGACAAAGACAC 997  
Db |||||||  
QY 931 AACTGAGACAGAAAGTGGAAATGAATACTCGGCTGACATTCAGATGACAAAGACAC 990  
Db |||||||  
QY 998 AGACACGGCTTCTCTCCCTCCCAATCTGTAATCCAGTGATCTCTGAAACAAAGAAACAG 1057  
Db |||||||  
QY 991 AGACACGGCTTCTCTCCCTCCCAATCTGTAATCCAGTGATCTCTGAAACAAAGAAACAG 1050  
Db |||||||  
QY 1058 TAGCTGTGGCCCTCTCACAGCGGGTGATCAACGTCTCACCGGCGAGCAAGTCAATCC 1117  
Db |||||||  
QY 1051 TAGCTGTGGCCCTCTCACAGCGGGTGATCAACGTCTCACCGGCGAGCAAGTCAATCC 1110  
Db |||||||  
QY 1118 ACAGGCTTCTTTAAATCTGGCCAGTCTGAGAGGTGAGTAATACACTGTAGTATAG 1175  
Db |||||||  
QY 1111 ACAGGCTTCTTTAAATCTGGCCAGTCTGAGAGGTGAGTAATACACTGTAGTATAG 1168  
Db |||||||

RESULT 5

ABK13031

ID ABK13031 standard; cDNA; 1139 BP.

AC ABK13031;

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Human; B7-like protein; B7-L; antiinfertility; gynaecological;  
antitumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic;  
antiinflammatory; dermatological; antipsoriatic; neuroprotective;  
antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic;  
antiaesthetic; nephrotoxic; antibacterial; virucide; tumour; cancer;  
reproductive disorder; graft versus host disease; autoimmune disease;  
toxic shock syndrome; allergy; nephropathy; skin disorder;  
endocrinopathy; lymphoproliferative disorder; gene; ss.

Homo sapiens.

Key Location/Qualifiers

FT 1..1134

FT /\*tag= a

FT /product= "B7-like protein, B7-L\_h4"

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polypeptide, polynucleotide encoding it and antibody against (I) are  
useful for treating B7-like polypeptide-related disease, disorders or  
conditions including reproductive disorders (e.g. infertility,  
miscarriage, preterm labour and delivery and endometriosis) and  
proliferative disorders. Antibodies, soluble proteins comprising  
extracellular domains and other regulators of B7-L polypeptides are  
useful for enhancing the immune response to tumours. (I) Plays a role in  
growth and maintenance of cancer cells based on the observation of  
seminal vesicle hyperplasia in transgenic mice overexpressing B7-L  
polypeptide. Hence modulators of (I) are useful for the treatment of  
cancer, including seminal vesicle cancer, lung, brain, breast, ovarian,  
testicular cancer and cancers of haematopoietic system. B7-L polypeptide  
pathway can be manipulated to regulate cytotoxic T-lymphocyte response in  
allotransplantation, graft versus host disease, T-cell dependent B-  
cell mediated diseases and autoimmune diseases. B7-L molecules are useful  
for alleviating the symptoms associated with diseases involving chronic  
immune cell dysfunction or to treat autoimmune diseases such as systemic  
lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes,  
immune thrombocytopenic purpura and psoriasis, chronic inflammatory  
disease such as inflammatory bowel disease (Crohn's disease and  
ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and  
diabetes mellitus). They are also useful as immunosuppressive agents for  
bone marrow and organ transplantation or to prolong graft survival. B7-L  
molecules are also useful for diagnosis and treatment of diseases  
involving abnormal cell proliferation, including arteriosclerosis and  
vascular restenosis. Antagonists of B7-L polypeptides are useful for  
alleviation of toxic shock syndrome or allergen sensitisation due to blood  
transfusions, and for treatment of allergy, asthma and hypersensitivity  
reactions, nephropathies (e.g. glomerulonephritis), skin disorders  
(pemphigus and pemphigoid), endocrinopathies (Grave's disease), various  
pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease,  
anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia  
gravis, and lymphoproliferative disorders such as multiple myeloma. The  
present sequence represents the coding sequence of human B7-L\_h4

Query Match 62.9%; Score 739; DB 6; Length 1139;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 789; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 98 AGTCCTGAAGGGCTCCAGGGCTCGCTTCAACTGCACCGTCTCCAGGGCTGGAAGTCAAT 157  
Db |||||||  
QY 84 AGTCCTGAAGGGCTCCAGGGCTCGCTTCAACTGCACCGTCTCCAGGGCTGGAAGTCAAT 143  
Db |||||||  
QY 158 CATGTGGGCTCTCAGTGACATGTTGGTCTAAGCGTCAGGCCCATGGAGCCCATCATCAC 217  
Db |||||||  
QY 144 CATGTGGGCTCTCAGTGACATGTTGGTCTAAGCGTCAGGCCCATGGAGCCCATCATCAC 203  
Db |||||||  
QY 218 CAATGACCGCTTACCTCTCAGAGTACGACGCGGGGAACTTCACTCGGAGATGAT 277  
Db |||||||  
QY 204 CAATGACCGCTTACCTCTCAGAGTACGACGCGGGGAACTTCACTCGGAGATGAT 263  
Db |||||||  
QY 278 CATCCACAATGTGGAGCCAGTGTTCGGGGAAACATCAGATGCGACCTCCAGAACAGTCG 337  
Db |||||||  
QY 264 CATCCACAATGTGGAGCCAGTGTTCGGGGAAACATCAGATGCGACCTCCAGAACAGTCG 323  
Db |||||||  
QY 338 CCTGATGGATCTGCTTACCTTACCGTCCAAAGTTATGGAGAGCTGTTTCATCCAGTGT 397  
Db |||||||  
QY 324 CCTGATGGATCTGCTTACCTTACCGTCCAAAGTTATGGAGAGCTGTTTCATCCAGTGT 383  
Db |||||||  
QY 398 TAATCTTGTAGTCGCTGAGATGAACCTTGTGAAGTTACTTGTCTACCTCAGCTGGAC 457  
Db |||||||  
QY 384 TAATCTTGTAGTCGCTGAGATGAACCTTGTGAAGTTACTTGTCTACCTCAGCTGGAC 443  
Db |||||||  
QY 458 CCGGCTCCCGGATATTTCTGGGAGCTCGGTCTCTCTGCTCAGCCATTCAAGCTATTATTT 517  
Db |||||||  
QY 444 CCGGCTCCCGGATATTTCTGGGAGCTCGGTCTCTCTGCTCAGCCATTCAAGCTATTATTT 503  
Db |||||||  
QY 518 TGTTCGGAGCCAGCGACCTTCAAAGTGCAGTGCATCTGGGCTCTGACCCACAGAG 577  
Db |||||||  
QY 504 TGTTCGGAGCCAGCGACCTTCAAAGTGCAGTGCATCTGGGCTCTGACCCACAGAG 563  
Db |||||||

New B7-like polypeptides, polynucleotides and their modulators, useful  
for diagnosing, preventing and treating reproductive, immune and  
proliferative disorders, e.g. cancer and arteriosclerosis.

Claim 1; Fig 4; 135pp; English.

The invention relates to an isolated B7-like (B7-L) polypeptide (I). The



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us-09-729-264-1.1.0lig.rng

ID ACH16130 standard; cDNA; 474 BP.  
 XX AC ACH16130;  
 XX DT 13-OCT-2003 (first entry)  
 XX DE Human adult heart cDNA #444.  
 XX KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
 XX KW genome mapping; biodiversity; genetic disorder.  
 XX OS Homo sapiens.  
 XX PN US2003073623-A1.  
 XX PD 17-APR-2003.  
 XX PF 30-JUL-2001; 2001US-00918995.  
 XX PR 30-JUL-2001; 2001US-00918995.  
 XX PA (DRMA/) DRMANAC R T.  
 XX PA (LABA/) LABAT I.  
 XX PA (STAC/) STACHE-CRAIN B.  
 XX PA (DICK/) DICKSON M C.  
 XX PA (JONE/) JONES L W.  
 XX PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
 XX PI WPI; 2003-615964/58.  
 XX DR New polynucleotide sequences obtained from various cDNA libraries, useful  
 XX PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
 XX PT mapping, in the recombinant production of protein, or in generating  
 XX PT antisense DNA or RNA.  
 XX PS Claim 1; SEQ ID NO 3342; 44pp; English.  
 XX CC The invention relates to an isolated polynucleotide comprising any one of  
 XX CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
 XX CC determined by the technique of SBH (sequencing by hybridisation). Also  
 XX CC included is a purified polypeptide comprising a sequence corresponding to  
 XX CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
 XX CC are useful in diagnostics as expressed sequence tags (EST) for  
 XX CC identifying expressed genes or for physical mapping of the human genome,  
 XX CC in forensics, in assessing biodiversity, or in identifying mutations  
 XX CC responsible for genetic disorders and other traits. The nucleotide  
 XX CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
 XX CC for chromosome and gene mapping, in the recombinant production of  
 XX CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
 XX CC is useful for generating antibodies specific for it. The present sequence  
 XX CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
 XX CC for this patent did not form part of the printed specification, but was  
 XX CC obtained in electronic format directly from USPTO at  
 XX CC seqdata.uspto.gov/sequence.html?DocID=20030073623  
 XX SQ Sequence 474 BP; 154 A; 128 C; 96 G; 95 T; 0 U; 1 Other;  
 Query Match 18.5%; Score 217; DB 8; Length 474;  
 Best Local Similarity 99.6%; Pred. No. 7.5e-98;  
 Matches 267; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 908 GAAATCTGAAAGAGACAAACAAAGAACTGAGACAGAAAGTGGAAATGAAATCTC 967  
 DB 63 GAAATCTGAAAGAGACAAACAAAGAACTGAGACAGAAAGTGGAAATGAAATCTC 122  
 QY 968 CGGCTACAAATTCAGATGAAACAAAGACACAGACACCGCTTCTCTCCCTCCCAATCTTG 1027  
 DB 123 CGGCTACAAATTCAGATGAAACAAAGACACAGACACCGCTTCTCTCCCTCCCAATCTTG 182  
 QY 1028 TGAATCCAGTGATCTTGAACAAAGAAACAGTAGCTGTGCGCTCTCCACACGGGGCTCA 1087  
 DB 183 TGAATCCAGTGATCTTGAACAAAGAAACAGTAGCTGTGCGCTCTCCACACGGGGCTCA 242  
 QY 1088 TCAAGCTCCACCCAGCCAGCAAGTCATCCACAGGCTTCTTTTAAATCTGGCCAGTCTCGA 1147  
 DB 243 TCAAGCTCCACCCAGCCAGCAAGTCATCCACAGGCTTCTTTTAAATCTGGCCAGTCTCGA 302  
 QY 1148 GAAGTTCAGTAATACAACTGTAGTAG 1175  
 DB 303 GAAGTTCAGTAATACAACTGTAGTAG 330  
 RESULT 8  
 AAI36582  
 ID AAI36582 standard; DNA; 401 BP.  
 XX AC AAI36582;  
 XX DT 17-OCT-2001 (first entry)  
 XX DE Probe #5268 used to measure gene expression in human placenta sample.  
 XX KW Probe; microarray; human; placenta; antenatal diagnosis;  
 XX KW genetic disorder; ss.  
 XX OS Homo sapiens.  
 XX PN WO200157272-A2.  
 XX PD 09-AUG-2001.  
 XX PF 30-JAN-2001; 2001WO-US000663.  
 XX PR 04-FEB-2000; 2000US-0180312P.  
 XX PR 26-MAY-2000; 2000US-0207456P.  
 XX PR 30-JUN-2000; 2000US-00608408.  
 XX PR 03-AUG-2000; 2000US-00632366.  
 XX PR 21-SEP-2000; 2000US-0234687P.  
 XX PR 27-SEP-2000; 2000US-0236359P.  
 XX PR 04-OCT-2000; 2000GB-00024263.  
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-488897/53.  
 XX DR Human genome-derived single exon nucleic acid probes useful for analyzing  
 XX PT gene expression in human placenta.  
 XX PS Claim 25; SEQ ID NO 5268; 654pp; English.  
 XX CC The present invention relates to single exon nucleic acid probes (SENP).  
 XX CC The present sequence is one such probe. The probes are useful for  
 XX CC producing a microarray for predicting, measuring and displaying gene  
 XX CC expression in samples derived from human placenta. The probes are useful  
 XX CC for antenatal diagnosis of human genetic disorders  
 XX SQ Sequence 401 BP; 105 A; 98 C; 111 G; 87 T; 0 U; 0 Other;  
 Query Match 12.3%; Score 144; DB 4; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-61;  
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 98 AGTCTGAGGGCTCCCGGCTTCGTTCAACTGCACCGCTCTCCAGGGCTGGAAGTCTAT 157  
 DB 258 AGTCTGAGGGCTCCCGGCTTCGTTCAACTGCACCGCTCTCCAGGGCTGGAAGTCTAT 317  
 QY 158 CATGTGGGCTCTCAGTCATGCTGCTGCTAAGCGTCAGGCCCATGGAGCCCATCATCAC 217  
 DB 318 CATGTGGGCTCTCAGTCATGCTGCTGCTAAGCGTCAGGCCCATGGAGCCCATCATCAC 377  
 QY 218 CAATGACCGCTTTCACCTCTCAGAG 241  
 DB 378 CAATGACCGCTTTCACCTCTCAGAG 401

RESULT 9  
 AAL04335  
 ID AAL04335 standard; DNA; 357 BP.  
 XX AC AAL04335;  
 XX DT 09-OCT-2001 (first entry)  
 XX DE Probe #4326 used to measure gene expression in human breast sample.  
 XX KW Probe; human; breast disease; breast cancer; development disorder; ss;  
 XX KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.  
 XX OS Homo sapiens.  
 XX PN WO200157270-A2.  
 XX PD 09-AUG-2001.  
 XX PF 29-JAN-2001; 2001WO-US000661.  
 XX PR 04-FEB-2000; 2000US-0180312P.  
 XX PR 26-MAY-2000; 2000US-0207456P.  
 XX PR 30-JUN-2000; 2000US-00608408.  
 XX PR 03-AUG-2000; 2000US-00632366.  
 XX PR 21-SEP-2000; 2000US-0234687P.  
 XX PR 27-SEP-2000; 2000US-0236359P.  
 XX PR 04-OCT-2000; 2000GB-00024263.  
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-476286/51.  
 XX PT Novel single exon nucleic acid probe used to measuring gene expression in  
 PT a human breast.  
 XX PS Claim 25; SEQ ID NO 4326; 322pp; English.  
 XX CC The present invention relates to novel single exon nucleic acid probes.  
 CC The present sequence is one such probe. The probes are useful for  
 CC measuring human gene expression in a human breast sample, where the probe  
 CC hybridises at high stringency to a nucleic acid expressed in the human  
 CC breast. The probes are useful for predicting, diagnosing, grading,  
 CC staging, monitoring and prognosing diseases of the human breast,  
 CC particularly those diseases with polygenic aetiology. The diseases  
 CC include: breast cancer, disorders of development, inflammatory diseases  
 CC of the breast, fibrocystic changes, proliferative breast disease and non-  
 CC carcinoma tumours. Note: The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 357 BP; 117 A; 68 C; 64 G; 108 T; 0 U; 0 Other;  
 Query Match 2.1%; Score 25; DB 5; Length 357;  
 Best Local Similarity 100.0%; Pred. No. 0.079;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 884 AGGATTTCGTATTCAATTTCAAAG 908  
 Db 42 AGGATTTCGTATTCAATTTCAAAG 66  
 RESULT 10  
 ABL15493/C  
 ID ABL15493 standard; cDNA; 6507 BP.  
 XX AC ABL15493;  
 XX DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 40961.  
 XX DE Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ss.  
 XX OS Drosophila melanogaster.  
 XX PN WO200171042-A2.  
 XX PD 27-SEP-2001.  
 XX PF 23-MAR-2001; 2001WO-US009231.  
 XX PR 23-MAR-2000; 2000US-0191637P.  
 XX PR 11-JUL-2000; 2000US-00614150.  
 XX PA (PEKE ) PE CORP NY.  
 XX PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX WPI; 2001-658860/75.  
 XX DR P-PSDB; ABB71390.  
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions.  
 XX PS Claim 1; SEQ ID NO 40961; 21pp + Sequence Listing; English.  
 XX CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-  
 CC ABBS72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 6507 BP; 1745 A; 1888 C; 1712 G; 1162 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 24; DB 4; Length 6507;  
 Best Local Similarity 100.0%; Pred. No. 0.26;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 807 CGCTGCTGCTGCTGCCGCCGCTCGT 830  
 Db 2946 CGCTGCTGCTGCTGCCGCCGCTCGT 2923  
 RESULT 11  
 ABL15492/C  
 ID ABL15492 standard; cDNA; 59967 BP.  
 XX AC ABL15492;  
 XX DT 26-MAR-2002 (first entry)  
 XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40958.  
 XX KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ss.  
 XX OS Drosophila melanogaster.  
 XX PN WO200171042-A2.  
 XX PD 27-SEP-2001.  
 XX PF 23-MAR-2001; 2001WO-US009231.  
 XX PS









CC that may affect the biological function of the gene or gene products.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from USPTO  
CC at seqdata.uspto.gov/sequence.html?DocID=99909770445  
XX  
SQ Sequence 767 BP; 169 A; 199 C; 147 G; 252 T; 0 U; 0 Other;  
  
Query Match 1.9%; Score 22; DB 6; Length 767;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 821 CGCGCGTCTGTTGTGGCTGC 842  
DB 672 CGCGCGTCTGTTGTGGCTGC 693  
  
Search completed: September 14, 2004, 23:41:47  
Job time : 508.04 secs

CC that may affect the biological function of the gene or gene products.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from USPTO  
CC at seqdata.uspto.gov/sequence.html?DocID=99909770445  
XX  
SQ Sequence 767 BP; 169 A; 199 C; 147 G; 252 T; 0 U; 0 Other;  
  
Query Match 1.9%; Score 22; DB 6; Length 767;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 821 CGCGCGTCTGTTGTGGCTGC 842  
DB 672 CGCGCGTCTGTTGTGGCTGC 693  
  
RESULT 15  
AAV5364  
ID AAV5364 standard; cDNA; 1200 BP.  
XX  
AC AAV5364;  
XX  
DT 28-SEP-1998 (first entry)  
XX  
DE Human GDNF alpha-3 receptor cDNA #1.  
XX  
KW Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;  
KW treatment; neurodegenerative disease; Parkinson's Disease; ALS; SMA;  
KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;  
KW Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;  
KW muscular dystrophy; diagnostic; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1200  
FT FT /\*tag= a  
FT FT /product= "GDNF alpha-3"  
FT FT /note= "partial sequence of glial cell-derived  
FT FT neurotrophic factor alpha-3 receptor"  
XX  
PN EP846764-A2.  
XX  
PD 10-JUN-1998.  
XX  
XX 20-NOV-1997; 97EP-00309375.  
XX  
XX 27-NOV-1996; 96GB-00024677.  
XX 09-MAY-1997; 97GB-00009463.  
XX  
XX (SMIK ) SMITHLINE BEECHAM PLC.  
XX  
XX Lawrence GMP;  
XX  
XX WPI; 1998-299980/27.  
XX P-PSDB; AAW65116.  
XX  
XX New factor alpha 3 receptor polypeptide and e.g. DNA and agonists - used  
XX to treat neuro degenerative diseases, muscular diseases and nerve and  
XX muscle trauma and in diagnostic assays.  
XX  
XX Claim 9; Fig 1; 22pp; English.  
XX  
XX This sequence encodes a novel glial cell line-derived neurotrophic factor  
XX alpha-3 receptor (GDNF alpha-3). This protein can be used to treat e.g.  
XX neurodegenerative diseases (such as Parkinson's Disease, amyotrophic  
XX lateral sclerosis (ALS), spinal muscular atrophy (SMA), Huntington's  
XX Disease, Alzheimer's Disease, diabetic neuropathy), muscular diseases  
XX (including the muscular dystrophies) and nerve and muscle trauma and in  
XX diagnostic assays for such conditions  
XX  
XX Sequence 1200 BP; 236 A; 419 C; 307 G; 238 T; 0 U; 0 Other;

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 23:14:24 ; Search time 91.8225 Seconds  
(without alignments)  
7101.389 Million cell updates/sec

Title: US-09-729-264-1

Perfect score: 1175

Sequence: 1 ctgtctgcccattctgaataa.....gtaatacaactgtagtatag 1175

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1281558

Minimum DB seq length: 16

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq.\*
- 2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/ina/PTUS.COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	1.9	1203	3	US-09-220-528-65
2	22	1.9	1699	4	US-09-187-906-20
3	22	1.9	3942	3	US-09-182-484-19
4	21	1.8	550	4	US-09-669-751-128
5	21	1.8	1428	4	US-09-489-039A-3243
6	20	1.7	394	4	US-09-621-976-16752
7	20	1.7	794	4	US-09-621-976-16751
8	20	1.7	984	4	US-09-252-991A-12897
9	20	1.7	1857	4	US-09-252-991A-12735
10	20	1.7	1910	3	US-09-593-711A-3
11	20	1.7	1914	1	US-07-601-094-1
12	20	1.7	1914	1	US-08-012-735-1
13	20	1.7	2214	3	US-08-864-038A-1
14	20	1.7	3331	3	US-08-864-038A-2
15	20	1.7	3331	3	US-08-864-038A-4
16	20	1.7	6407	2	US-08-616-844-7
17	20	1.7	6407	2	US-08-599-654-7
18	20	1.7	6407	3	US-08-944-868A-7
19	20	1.7	6407	3	US-08-944-423A-7
20	20	1.7	6407	3	US-08-944-496-7
21	19	1.6	402	4	US-09-621-976-88
22	19	1.6	1425	1	US-08-464-148-1
23	19	1.6	1425	1	US-08-385-500-1
24	19	1.6	1425	1	US-08-846-784-1
25	19	1.6	1477	4	US-09-620-312D-1019
26	19	1.6	1768	4	US-09-833-381-523
27	19	1.6	1899	4	US-09-919-060-15

C	28	19	1.6	1899	4	US-09-919-060-16	Sequence 16, Appl
	29	19	1.6	1889	1	US-08-447-500-5	Sequence 5, Appl
	30	19	1.6	1889	1	US-08-454-097-5	Sequence 5, Appl
	31	19	1.6	1889	1	US-08-453-866-5	Sequence 5, Appl
	32	19	1.6	1889	3	US-08-185-359-5	Sequence 5, Appl
	33	19	1.6	1995	4	US-09-620-312D-908	Sequence 908, App
	34	19	1.6	2023	4	US-09-491-522-6	Sequence 6, Appl
	35	19	1.6	2115	2	US-08-474-379C-60	Sequence 60, Appl
	36	19	1.6	2115	3	US-09-146-249A-60	Sequence 60, Appl
	37	19	1.6	2115	3	US-08-206-188B-60	Sequence 60, Appl
	38	19	1.6	2439	4	US-09-489-039A-4904	Sequence 4904, Ap
	39	19	1.6	2450	4	US-09-491-522-2	Sequence 2, Appl
	40	19	1.6	2617	4	US-09-786-240-21	Sequence 21, Appl
	41	19	1.6	2693	4	US-09-919-060-12	Sequence 12, Appl
	42	19	1.6	2693	4	US-09-919-060-14	Sequence 14, Appl
	43	19	1.6	3311	4	US-09-367-891A-5	Sequence 5, Appl
	44	19	1.6	5092	3	US-09-412-545-1	Sequence 1, Appl
	45	19	1.6	5621	4	US-09-566-921-106	Sequence 106, App

## ALIGNMENTS

RESULT 1  
US-09-220-528-65  
; Sequence 65, Application US/09220528A  
; Patent No. 6284540  
; GENERAL INFORMATION:  
; APPLICANT: Milbrandt, Jeffrey D.  
; APPLICANT: Baloh, Robert H.  
; TITLE OF INVENTION: Artemin, A No. 6284540e1 Neurotrophic Factor  
; FILE REFERENCE: 6029-7998  
; CURRENT APPLICATION NUMBER: US/09/220,528A  
; CURRENT FILING DATE: 1998-12-24  
; EARLIER APPLICATION NUMBER: 09/218,698  
; EARLIER FILING DATE: 1998-12-22  
; EARLIER APPLICATION NUMBER: 60/108,148  
; EARLIER FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: 09/163,283  
; EARLIER FILING DATE: 1998-09-29  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 65  
; LENGTH: 1203  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-220-528-65

Query Match 1.9%; Score 22; DB 3; Length 1203;  
Best Local Similarity 100.0%; Pred. No. 0.17;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 808 GCGCTGCTGCTGCGCGCGTCG 829  
Db 51 GCGCTGCTGCTGCGCGCGTCG 72

RESULT 2  
US-09-187-906-20  
; Sequence 20, Application US/09187906  
; Patent No. 6677135  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC.  
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural  
; TITLE OF INVENTION: and Renal Growth  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Biogen, Inc.  
; STREET: 14 Cambridge Center  
; CITY: Cambridge  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02142

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/187,906  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/07726  
FILING DATE: 07-MAY-97  
APPLICATION NUMBER: US 60/017,427  
FILING DATE: 08-MAY-96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/019,300  
FILING DATE: 07-JUN-96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/021,859  
FILING DATE: 16-JUL-96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/043,533  
FILING DATE: 10-APR-97  
ATTORNEY/AGENT INFORMATION:  
NAME: Kaplan, Warren A.  
REGISTRATION NUMBER: 34,199  
REFERENCE/DOCKET NUMBER: A008 PCT CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-679-2400  
TELEFAX: 617-679-2838  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1699 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 175..1374  
US-09-187-906-20

Query Match 1.9%; Score 22; DB 4; Length 1699;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 808 GCTGCTGCTGCTGCGCGCTCG 829  
DB 225 GCTGCTGCTGCTGCGCGCTCG 246

RESULT 3  
US-09-162-484-19  
Sequence 19, Application US/09162484  
Patent No. 6248724  
GENERAL INFORMATION:  
APPLICANT: Phillips, M. Ian  
APPLICANT: Mohuczy, Dagmara  
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS TARGETED TO  
FILE REFERENCE: UFLA:087/UFLA087P  
CURRENT APPLICATION NUMBER: US/09/162,484  
CURRENT FILING DATE: 1998-09-25  
EARLIER APPLICATION NUMBER: 60/059,661  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 19  
LENGTH: 3942  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-09-162-484-19

Query Match 1.9%; Score 22; DB 4; Length 1699;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 808 GCTGCTGCTGCTGCGCGCTCG 829  
DB 225 GCTGCTGCTGCTGCGCGCTCG 246

RESULT 4  
US-09-669-751-128/c  
Sequence 128, Application US/09669751  
Patent No. 6551575  
GENERAL INFORMATION:  
APPLICANT: Greenspan, Ralph J.  
TITLE OF INVENTION: Methods for Identifying Compounds for  
TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to  
TITLE OF INVENTION: Balance and the Perception of Gravity  
FILE REFERENCE: P-NI 3864  
CURRENT APPLICATION NUMBER: US/09/669,751  
PRIOR FILING DATE: 2000-09-26  
PRIOR FILING DATE: 1999-12-02  
NUMBER OF SEQ ID NOS: 261  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 128  
LENGTH: 550  
TYPE: DNA  
ORGANISM: Drosophila  
US-09-669-751-128

Query Match 1.8%; Score 21; DB 4; Length 550;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 844 ACTGCTGCTGCTGCTGTT 864  
DB 317 ACTGCTGCTGCTGCTGTT 297

RESULT 5  
US-09-489-039A-3243/c  
Sequence 3243, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
FILE REFERENCE: 2709-2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 3243  
LENGTH: 1428  
TYPE: DNA  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-3243

Query Match 1.8%; Score 21; DB 4; Length 1428;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GCTTCAACTGCACCGCTCTCCC 141  
DB 1147 GCTTCAACTGCACCGCTCTCCC 1127

RESULT 6  
US-09-621-976-16752  
Sequence 16752, Application US/09621976  
Patent No. 6639063

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/187,906  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/07726  
FILING DATE: 07-MAY-97  
APPLICATION NUMBER: US 60/017,427  
FILING DATE: 08-MAY-96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/019,300  
FILING DATE: 07-JUN-96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/021,859  
FILING DATE: 16-JUL-96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/043,533  
FILING DATE: 10-APR-97  
ATTORNEY/AGENT INFORMATION:  
NAME: Kaplan, Warren A.  
REGISTRATION NUMBER: 34,199  
REFERENCE/DOCKET NUMBER: A008 PCT CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-679-2400  
TELEFAX: 617-679-2838  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1699 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 175..1374  
US-09-187-906-20

Query Match 1.9%; Score 22; DB 4; Length 1699;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 808 GCTGCTGCTGCTGCGCGCTCG 829  
DB 225 GCTGCTGCTGCTGCGCGCTCG 246

RESULT 3  
US-09-162-484-19  
Sequence 19, Application US/09162484  
Patent No. 6248724  
GENERAL INFORMATION:  
APPLICANT: Phillips, M. Ian  
APPLICANT: Mohuczy, Dagmara  
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS TARGETED TO  
FILE REFERENCE: UFLA:087/UFLA087P  
CURRENT APPLICATION NUMBER: US/09/162,484  
CURRENT FILING DATE: 1998-09-25  
EARLIER APPLICATION NUMBER: 60/059,661  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 19  
LENGTH: 3942  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-09-162-484-19

Query Match 1.9%; Score 22; DB 4; Length 1699;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 808 GCTGCTGCTGCTGCGCGCTCG 829  
DB 225 GCTGCTGCTGCTGCGCGCTCG 246

RESULT 4  
US-09-669-751-128/c  
Sequence 128, Application US/09669751  
Patent No. 6551575  
GENERAL INFORMATION:  
APPLICANT: Greenspan, Ralph J.  
TITLE OF INVENTION: Methods for Identifying Compounds for  
TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to  
TITLE OF INVENTION: Balance and the Perception of Gravity  
FILE REFERENCE: P-NI 3864  
CURRENT APPLICATION NUMBER: US/09/669,751  
PRIOR FILING DATE: 2000-09-26  
PRIOR FILING DATE: 1999-12-02  
NUMBER OF SEQ ID NOS: 261  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 128  
LENGTH: 550  
TYPE: DNA  
ORGANISM: Drosophila  
US-09-669-751-128

Query Match 1.8%; Score 21; DB 4; Length 550;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 844 ACTGCTGCTGCTGCTGTT 864  
DB 317 ACTGCTGCTGCTGCTGTT 297

RESULT 5  
US-09-489-039A-3243/c  
Sequence 3243, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
FILE REFERENCE: 2709-2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 3243  
LENGTH: 1428  
TYPE: DNA  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-3243

Query Match 1.8%; Score 21; DB 4; Length 1428;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GCTTCAACTGCACCGCTCTCCC 141  
DB 1147 GCTTCAACTGCACCGCTCTCCC 1127

RESULT 6  
US-09-621-976-16752  
Sequence 16752, Application US/09621976  
Patent No. 6639063

; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 16752  
; LENGTH: 394  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-621-976-16752

Query Match 1.7%; Score 20; DB 4; Length 394;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 817 GCTGCCGCCGCTGTTGTTGT 836  
DB 34 GCTGCCGCCGCTGTTGTTGT 53

RESULT 7  
US-09-621-976-16751  
; Sequence 16751, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 16751  
; LENGTH: 794  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-621-976-16751

Query Match 1.7%; Score 20; DB 4; Length 794;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 817 GCTGCCGCCGCTGTTGTTGT 836  
DB 34 GCTGCCGCCGCTGTTGTTGT 53

RESULT 8  
US-09-252-991A-12897  
; Sequence 12897, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 12897  
; LENGTH: 984  
; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-12897

Query Match 1.7%; Score 20; DB 4; Length 984;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 834 TGTGGCTGCAACTGCTGCTG 853  
DB 395 TGTGGCTGCAACTGCTGCTG 414

RESULT 9  
US-09-252-991A-12735  
; Sequence 12735, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 12735  
; LENGTH: 1857  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-12735

Query Match 1.7%; Score 20; DB 4; Length 1857;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 834 TGTGGCTGCAACTGCTGCTG 853  
DB 1746 TGTGGCTGCAACTGCTGCTG 1765

RESULT 10  
US-09-593-711A-3/c  
; Sequence 3, Application US/09593711A  
; Patent No. 6271030  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Madeline M. Butler  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION  
; FILE REFERENCE: RTS-0118  
; CURRENT APPLICATION NUMBER: US/09/593,711A  
; CURRENT FILING DATE: 2000-06-14  
; NUMBER OF SEQ ID NOS: 244  
; SEQ ID NO 3  
; LENGTH: 1910  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION:  
; NAME/KEY: unsure  
; LOCATION: 1415  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 1421  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 1422  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 1423

Wed Sep 15 10:41:06 2004

us-09-729-264-1-olig.rni

OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 1424  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 1458  
OTHER INFORMATION: unknown  
NAME/KEY: CDS  
LOCATION: (299) ... (1336)  
US-09-593-711A-3

Query Match 1.7%; Score 20; DB 3; Length 1910;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 807 CGCTGCTGCTGCTGCGCGCG 826  
DB 205 CGCTGCTGCTGCTGCGCGCG 186

RESULT 11  
US-07-601-094-1/c  
Sequence 1, Application US/07601094  
Patent No. 5215892  
GENERAL INFORMATION:  
APPLICANT: Kishimoto, Tadimitsu  
APPLICANT: Hirano, Toshio  
APPLICANT: Akira, Shizuo  
APPLICANT: Isshiki, Hiroshi  
APPLICANT: Tanabe, Osamu  
APPLICANT: Kinoshita, Shigemi  
APPLICANT: Shimamoto, Takuya  
TITLE OF INVENTION: C/EBP2 Gene and Recombinant  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak &  
ADDRESSEE: Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/601,094  
FILING DATE: 19901022  
CLASSIFICATION: 435  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1914 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 281..1316  
OTHER INFORMATION:

Query Match 1.7%; Score 20; DB 1; Length 1914;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 807 CGCTGCTGCTGCTGCGCGCG 826  
DB 204 CGCTGCTGCTGCTGCGCGCG 185

RESULT 12  
US-08-012-735-1/c  
Sequence 1, Application US/08012735  
Patent No. 5360894  
GENERAL INFORMATION:  
APPLICANT: Kishimoto, Tadimitsu  
APPLICANT: Hirano, Toshio  
APPLICANT: Akira, Shizuo  
APPLICANT: Isshiki, Hiroshi  
APPLICANT: Tanabe, Osamu  
APPLICANT: Kinoshita, Shigemi  
APPLICANT: Shimamoto, Takuya  
TITLE OF INVENTION: C/EBP2 Gene and Recombinant  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak &  
ADDRESSEE: Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/012,735  
FILING DATE: 19930203  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/601,094  
FILING DATE: 22 OCT 1990  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1914 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 281..1316  
OTHER INFORMATION:

Query Match 1.7%; Score 20; DB 1; Length 1914;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 807 CGCTGCTGCTGCTGCGCGCG 826  
DB 204 CGCTGCTGCTGCTGCGCGCG 185

RESULT 13  
US-08-864-038A-1  
Sequence 1, Application US/08864038A  
Patent No. 6001592  
GENERAL INFORMATION:  
APPLICANT: Kunio NAKASHIMA et al.  
TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE cDNA, VECTOR

;; TITLE OF INVENTION: CONTAINING SAID cDNA, HOST CELLS TRANSFORMED WITH SAID  
;; TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING  
;; TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY  
;; TITLE OF INVENTION: TO SAID POLYPEPTIDE  
;; NUMBER OF SEQUENCES: 4  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: 812-5 Hirano  
;; STREET: Isshinden  
;; CITY: Tsu-city  
;; STATE: Mie-prefecture  
;; COUNTRY: JAPAN  
;; ZIP: 514-01  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: Microsoft Windows 95  
;; SOFTWARE: Word Perfect 6.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/864,038A  
;; FILING DATE: May 28, 1997  
;; PRIORITY APPLICATION DATA:  
;; APPLICATION NUMBER: JP 8-184459  
;; FILING DATE: 15-July-1996  
;; NAME: C. Bruce Hamburg  
;; REGISTRATION NUMBER: 22,389  
;; REFERENCE/DOCKET NUMBER: F-5610  
;; TELEPHONE: (212)986-2340  
;; TELEFAX: (212)953-7733  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2214  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; ORGANISM: Pinctada fucata  
;; CELL TYPE: mantle epithelial cell  
US-08-864-038A-1

Query Match 1.7%; Score 20; DB 3; Length 2214;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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; Sequence 2, Application US/08864038A  
; Patent No. 6001592  
; GENERAL INFORMATION:  
; APPLICANT: Kunio NAKASHIMA et al.  
; TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE cDNA, VECTOR  
; TITLE OF INVENTION: CONTAINING SAID cDNA, HOST CELLS TRANSFORMED WITH SAID  
; TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING  
; TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: 812-5 Hirano  
; STREET: Isshinden  
; CITY: Tsu-city  
; STATE: Mie-prefecture  
; COUNTRY: JAPAN  
; ZIP: 514-01  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Microsoft Windows 95

;; SOFTWARE: Word Perfect 6.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/864,038A  
;; FILING DATE: May 28, 1997  
;; PRIORITY APPLICATION DATA:  
;; APPLICATION NUMBER: JP 8-184459  
;; FILING DATE: 15-July-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: C. Bruce Hamburg  
;; REGISTRATION NUMBER: 22,389  
;; REFERENCE/DOCKET NUMBER: F-5610  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212)986-2340  
;; TELEFAX: (212)953-7733  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 3331  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA to mRNA  
;; ORIGINAL SOURCE:  
;; ORGANISM: Pinctada fucata  
;; CELL TYPE: mantle epithelial cell  
;; FEATURE: mRNA  
;; LOCATION: from 1 to 3331  
;; IDENTIFICATION METHOD: E (by experiment)  
US-08-864-038A-2  
  
Query Match 1.7%; Score 20; DB 3; Length 3331;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 807 CGTGTCTGCTGCTGCCGCG 826  
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Db 904 CGTGTCTGCTGCTGCCGCG 923  
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RESULT 15  
US-08-864-038A-4  
; Sequence 4, Application US/08864038A  
; Patent No. 6001592  
; GENERAL INFORMATION:  
; APPLICANT: Kunio NAKASHIMA et al.  
; TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE cDNA, VECTOR  
; TITLE OF INVENTION: CONTAINING SAID cDNA, HOST CELLS TRANSFORMED WITH SAID  
; TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING  
; TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: 812-5 Hirano  
; STREET: Isshinden  
; CITY: Tsu-city  
; STATE: Mie-prefecture  
; COUNTRY: JAPAN  
; ZIP: 514-01  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Microsoft Windows 95  
; SOFTWARE: Word Perfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/864,038A  
; FILING DATE: May 28, 1997  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: JP 8-184459  
; FILING DATE: 15-July-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: C. Bruce Hamburg  
; REGISTRATION NUMBER: 22,389  
; REFERENCE/DOCKET NUMBER: F-5610  
; TELECOMMUNICATION INFORMATION:

us-09-729-264-1.olig.rni

Wed Sep 15 10:41:06 2004

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; TELEPHONE: (212)986-2340
; TELEFAX: (212)953-7733
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 3331
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA to mRNA
;   ORIGINAL SOURCE:
;     ORGANISM: Pinctada fucata
;     CELL TYPE: mantle epithelial cell
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: from 50 to 2263
;     IDENTIFICATION METHOD: P (by similarity to some other pattern)
; US-08-864-038A-4

Query Match      1.7%  Score 20; DB 3; Length 3331;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      807 CGCTGCTGCTGCTGCTGCCGCCG 826
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Db      904 CGCTGCTGCTGCTGCTGCCGCCG 923

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Job time : 92.8225 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 23:16:34 ; Search time 624.393 Seconds  
(without alignments)  
9468.459 Million cell updates/sec

Title: US-09-729-264-1

Perfect score: 1175

Sequence: 1 cgtgtgcccattgaataa.....gtaatacaactgtatagat 1175

Scoring table: OLIGO.NUC

Gapop 60.0 , Gapext 60.0

Searched: 3304383 seqs, 2515761380 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6509420

Minimum DB seq length: 16

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1076	91.6	2051	16	US-10-104-047-1104
2	217	18.5	474	10	US-09-918-995-3342
3	144	12.3	401	9	US-09-864-761-16305
4	25	2.1	357	9	US-09-864-761-16653
5	23	2.0	1284	17	US-10-437-963-81852
6	22	1.9	767	9	US-09-770-445-930
7	22	1.9	1203	9	US-09-220-920-65
8	22	1.9	1829	9	US-09-828-366-15
9	22	1.9	4142	12	US-10-152-319A-1498
10	21	1.8	462	17	US-10-437-963-41506
11	21	1.8	493	10	US-09-918-995-11051
12	21	1.8	550	15	US-10-255-536-128
13	21	1.8	602	17	US-10-767-701-28842
14	21	1.8	1558	10	US-09-930-213-20
					Sequence 1104, Ap
					Sequence 3342, Ap
					Sequence 16305, A
					Sequence 16653, A
					Sequence 81852, A
					Sequence 930, App
					Sequence 65, Appl
					Sequence 15, Appl
					Sequence 1498, Ap
					Sequence 41506, A
					Sequence 11051, A
					Sequence 128, App
					Sequence 28842, A
					Sequence 20, Appl

C 15	21	1.8	3362	13	US-10-087-192-185	Sequence 185, App
C 16	21	1.8	94917	13	US-10-087-192-184	Sequence 184, App
C 17	20	1.7	330	17	US-10-437-963-55684	Sequence 55684, A
C 18	20	1.7	358	13	US-09-823-245A-58	Sequence 58, Appl
C 19	20	1.7	398	9	US-09-983-965-4945	Sequence 4945, Ap
C 20	20	1.7	412	10	US-09-918-995-5855	Sequence 5855, Ap
C 21	20	1.7	507	17	US-10-430-201-970	Sequence 970, App
C 22	20	1.7	507	17	US-10-430-201-971	Sequence 971, App
C 23	20	1.7	596	17	US-10-767-701-5378	Sequence 5378, Ap
C 24	20	1.7	848	13	US-10-425-114-20418	Sequence 20418, A
C 25	20	1.7	863	13	US-10-027-632-150405	Sequence 150405, A
C 26	20	1.7	863	16	US-10-027-632-150405	Sequence 150405, A
C 27	20	1.7	1192	16	US-10-120-988-90	Sequence 90, Appl
C 28	20	1.7	1255	13	US-10-425-114-19266	Sequence 19266, A
C 29	20	1.7	1290	15	US-10-146-733-16	Sequence 16, Appl
C 30	20	1.7	1383	17	US-10-437-963-37464	Sequence 37464, A
C 31	20	1.7	1526	13	US-10-425-114-31002	Sequence 31002, A
C 32	20	1.7	1576	13	US-09-852-386-87	Sequence 87, Appl
C 33	20	1.7	1814	15	US-10-060-036-182	Sequence 182, App
C 34	20	1.7	1910	9	US-09-789-836-1	Sequence 1, Appl
C 35	20	1.7	1910	10	US-09-789-831-1	Sequence 1, Appl
C 36	20	1.7	1910	17	US-10-415-325-18	Sequence 18, Appl
C 37	20	1.7	1943	15	US-10-146-733-14	Sequence 14, Appl
C 38	20	1.7	2080	13	US-10-257-022-30	Sequence 30, Appl
C 39	20	1.7	2504	14	US-10-108-605-246	Sequence 246, App
C 40	20	1.7	2616	17	US-10-437-963-75800	Sequence 75800, A
C 41	20	1.7	2874	9	US-09-801-260-3	Sequence 3, Appl
C 42	20	1.7	2874	15	US-10-145-586-42	Sequence 42, Appl
C 43	20	1.7	3112	16	US-10-120-988-261	Sequence 261, App
C 44	20	1.7	3226	9	US-09-801-260-1	Sequence 1, Appl
C 45	20	1.7	3226	15	US-10-145-586-40	Sequence 40, Appl

#### ALIGNMENTS

RESULT 1  
US-10-104-047-1104  
; Sequence 1104, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA  
; FILE REFERENCE: HI-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1104  
; LENGTH: 2051  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-104-047-1104

Query Match 91.6%; Score 1076; DB 16; Length 2051;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1126; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 49 ACGTTCTGGTCTGTAATGAAGTCATAGAGGCCGCCAGATGCAAGTCTCTGAAG 108  
DB 201 ACGTTCTGGTCTGTAATGAAGTCATAGAGGCCGCCAGATGCAAGTCTCTGAAG 260  
QY 109 GCTCCAGGCTCGCTTCAACTGCACCGTCTCCAGGGCTGGAAGCTCATCATGGGCTC 168  
DB 261 GCTCCAGGCTCGCTTCAACTGCACCGTCTCCAGGGCTGGAAGCTCATCATGGGCTC 320  
QY 169 TCAGTGACATGTGGTGTAAAGCGTCAGGCCCATCATCAATGACCGGT 228  
DB 321 TCAGTGACATGTGGTGTAAAGCGTCAGGCCCATCATCAATGACCGGT 380  
QY 229 TCACCTCTCAGAGGTACGACACAGGGGGGAATCTCACCTCGGAGATGATCATCCCAATG 288



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; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16305
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF121782.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
US-09-864-761-16305

Query Match      12.3%; Score 144; DB 9; Length 401;
Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 AGTCCTGAAGGGCTCCAGGCTCCCACTGACCGCTCTCCAGGCTGGAGGCTCAT 157
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QY 158 CAGTGGGGCTCTCAGTGACATGTTGGTGAAGCGTCAGGCCCATGGAGCCCATCATCAC 217
Db 318 CAGTGGGGCTCTCAGTGACATGTTGGTGAAGCGTCAGGCCCATGGAGCCCATCATCAC 377

QY 218 CAATGACCGCTTCACCTCTCAGAG 241
Db 378 CAATGACCGCTTCACCTCTCAGAG 401

RESULT 4
US-09-864-761-16653
; Sequence 16653, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16653
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF064857.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.93
US-09-864-761-16653

Query Match      2.1%; Score 25; DB 9; Length 357;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 42 AGGATTTCGTATTCAATTTCAAAAG 66

RESULT 5
US-10-437-963-81852/c
; Sequence 81852, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 81852
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_81337C.1
US-10-437-963-81852

Query Match      2.0%; Score 23; DB 17; Length 1284;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	807	CGCTGCTGCTGCTGCGCGCTGC	829		
DB	156	CGCTGCTGCTGCTGCGCGCTGC	134		
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US-09-770-445-930					
; Sequence 930, Application US/09770445					
; Patent No. US20020023281A1					
; GENERAL INFORMATION:					
; APPLICANT: Gorlach, Jorn					
; APPLICANT: An, Yong-Qiang					
; APPLICANT: Hamilton, Carol M.					
; APPLICANT: Price, Jennifer L.					
; APPLICANT: Raines, Tracy M.					
; APPLICANT: Yu, Yang					
; APPLICANT: Rameaka, Joshua G.					
; APPLICANT: Page, Amy					
; APPLICANT: Matthew, Abraham V.					
; APPLICANT: Ledford, Brooke L.					
; APPLICANT: Woessner, Jeffrey P.					
; APPLICANT: Haas, William David					
; APPLICANT: Garcia, Carlos A.					
; APPLICANT: Kricker, Maja					
; APPLICANT: Slader, Ted					
; APPLICANT: Davis, Keith R.					
; APPLICANT: Allen, Keith					
; APPLICANT: Hoffman, Neil					
; APPLICANT: Hurlan, Patrick					
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis					
; TITLE OF INVENTION: thaliana					
; FILE REFERENCE: 2023US (PARA-012PRV)					
; CURRENT APPLICATION NUMBER: US/09/770,445					
; CURRENT FILING DATE: 2001-01-26					
; PRIOR APPLICATION NUMBER: US 60/178,472					
; PRIOR FILING DATE: 2000-01-27					
; NUMBER OF SEQ ID NOS: 999					
; SOFTWARE: FastSeq for Windows Version 4.0					
; SEQ ID NO 930					
; LENGTH: 767					
; TYPE: DNA					
; ORGANISM: Arabidopsis thaliana					
US-09-770-445-930					
Query Match 1.9%; Score 22; DB 9; Length 767;					
Best Local Similarity 100.0%; Pred.No. 1.5;					
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	821	CGCCGCTGCTGCTTGTGCTGC	842		
DB	672	CGCCGCTGCTGCTTGTGCTGC	693		
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; Sequence 65, Application US/09220920					
; Patent No. US20020002269A1					
; GENERAL INFORMATION:					
; APPLICANT: Milbrandt, Jeffrey D.					
; APPLICANT: Baloh, Robert H.					
; TITLE OF INVENTION: Artemin, A No. US20020002269A1el Neurotrophic Factor					
; FILE REFERENCE: 6029-7996					
; CURRENT APPLICATION NUMBER: US/09/220,920					
; CURRENT FILING DATE: 1998-12-24					
; EARLIER APPLICATION NUMBER: 09/163,283					
; EARLIER FILING DATE: 1998-09-29					
; EARLIER APPLICATION NUMBER: 60/108,148					
; EARLIER FILING DATE: 1998-11-12					
; EARLIER APPLICATION NUMBER: 09/219,698					
; EARLIER FILING DATE: 1998-12-22					
; NUMBER OF SEQ ID NOS: 120					

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; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/330,462
; PRIOR FILING DATE: 2001-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1498
; LENGTH: 4142
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_012544
US-10-152-319A-1498

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 808 GCTGCTGCTGCGCGCGTCG 829
Db 95 GCTGCTGCTGCGCGCGTCG 116

RESULT 10
US-10-437-963-41506/c
; Sequence 41506, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)/B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 41506
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_44844C.1
US-10-437-963-41506

Query Match
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 809 CTGCTGCTGCTGCGCGTCG 829
Db 133 CTGCTGCTGCTGCGCGTCG 113

RESULT 11
US-09-918-995-11051/c
; Sequence 11051, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
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; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11051
; LENGTH: 493
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(493)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-11051

Query Match
Best Local Similarity 1.8%; Score 21; DB 10; Length 493;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 811 GCTGCTGCTGCGCGCGTCGTT 831
Db 443 GCTGCTGCTGCGCGCGTCGTT 423

RESULT 12
US-10-255-536-128/c
; Sequence 128, Application US/10255536
; Publication No. US20030087807A1
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Ralph J.
; TITLE OF INVENTION: Methods for Identifying Compounds for
; TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to
; TITLE OF INVENTION: Balance and the Perception of Gravity
; FILE REFERENCE: P-NI 3864
; CURRENT APPLICATION NUMBER: US/10/255,536
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US/09/669,751
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 60/168,579
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Drosophila
; OTHER INFORMATION:
US-10-255-536-128

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 844 ACTGCTGCTGCGCGTCGTTGTT 864
Db 317 ACTGCTGCTGCGCGTCGTTGTT 297

RESULT 13
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; Sequence 28842, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
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Wed Sep 15 10:41:06 2004

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; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 28842
; LENGTH: 602
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 8088472
US-10-767-701-28842

Query Match      1.8%; Score 21; DB 17; Length 602;
Best Local Similarity 100.0%; Pred.No. 5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 810 TGCTGCTGCTGCCGCGTGT 830
Db 206 TGCTGCTGCTGCCGCGTGT 186

RESULT 14
US-09-930-213-20/c
; Sequence 20, Application US/09930213
; Publication No. US20030170625A1
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, ANDRE
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHAFER, REINHARD
; APPLICANT: ZUBER, JOHANNES
; APPLICANT: TCHE-NITSE, OLEG
; APPLICANT: GRIPS, MARTIN
; APPLICANT: HELLMER, MARTIN
; APPLICANT: SCHMITZ, ANNE-CHANTAL
; APPLICANT: SERS, CHRISTINE
; TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS
; FILE REFERENCE: ALBRE-14
; CURRENT APPLICATION NUMBER: US/09/930,213
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: DE 10004102.7
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 885
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 1558
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (16)
; OTHER INFORMATION: a, t, c, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (427)
; OTHER INFORMATION: a, t, c, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (492)
; OTHER INFORMATION: a, t, c, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (551)
; OTHER INFORMATION: a, t, c, g, other or unknown
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; NAME/KEY: modified_base
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; OTHER INFORMATION: a, t, c, g, other or unknown
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; LOCATION: (979)

OTHER INFORMATION: a, t, c, g, other or unknown
FEATURE:
NAME/KEY: modified_base
LOCATION: (1146)
OTHER INFORMATION: a, t, c, g, other or unknown
FEATURE:
NAME/KEY: modified_base
LOCATION: (1243)
OTHER INFORMATION: a, t, c, g, other or unknown
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LOCATION: (1343)
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FEATURE:
NAME/KEY: modified_base
LOCATION: (1346)
OTHER INFORMATION: a, t, c, g, other or unknown
FEATURE:
NAME/KEY: modified_base
LOCATION: (1352)
OTHER INFORMATION: a, t, c, g, other or unknown
FEATURE:
NAME/KEY: modified_base
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OTHER INFORMATION: a, t, c, g, other or unknown
FEATURE:
NAME/KEY: modified_base
LOCATION: (1535)
OTHER INFORMATION: a, t, c, g, other or unknown
US-09-930-213-20

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Best Local Similarity 100.0%; Pred.No. 5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 808 GCTGCTGCTGCTGCCGCGTC 828
Db 223 GCTGCTGCTGCTGCCGCGTC 203

RESULT 15
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; Sequence 185, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185
; LENGTH: 3362
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-087-192-185

Query Match      1.8%; Score 21; DB 13; Length 3362;
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Qy 808 GCTGCTGCTGCTGCCGCGTC 828
Db 947 GCTGCTGCTGCTGCCGCGTC 927
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Wed Sep 15 10:41:06 2004

us-09-729-264-1.olig.rnpb

Page 7

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Job time : 626.393 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Searched: 3470272 seqs, 21671516995 residues

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Post-processing: Listing first 45 summaries

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40: em\_hlgo\_mus.\*

41: em\_hlgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	1027	87.9	1175	6	AX380396	AX380396 Sequence
3	976	83.6	1240	6	AX380400	AX380400 Sequence
4	976	83.6	2051	6	AX747579	AX747579 Sequence
5	976	83.6	2051	6	AX092516	AX092516 Homo sapi
6	771	66.0	1139	6	AX380402	AX380402 Sequence
7	319	27.3	142742	9	AF121782	AF121782 Homo sapi
8	319	27.3	340000	9	HS21C080	AL163280 Homo sapi
9	241	20.6	182532	9	CH179K04	AL954228 Homo sapi
10	145	12.4	156288	9	BS000162	BS000162 Pan trogl
11	100	8.6	199665	9	AF064857	AF064857 Homo sapi
12	72	6.2	192219	9	RF43002119	AL954227 Pan trogl
13	40	3.4	170121	9	AF064860	AF064860 Homo sapi
14	25	2.1	6470	3	AB090820	AB090820 Anopheles
15	24	2.1	5178	3	AY119603	AY119603 Drosophila
16	24	2.1	8152	3	DMTOC	Y14157 Drosophila
17	24	2.1	77137	3	AC004422	AC004422 Drosophila
18	24	2.1	83876	2	AC020009	AC020009 Drosophila
19	24	2.1	148102	8	AF003328	AP003328 Oryza sat
20	24	2.1	148762	8	AF002843	AP002843 Oryza sat
21	24	2.1	169931	3	AC008321	AC008321 Drosophila
22	24	2.1	184554	3	AC095022	AC095022 Drosophila
23	24	2.1	268984	3	AE001274	AE001274 Leishmani
24	24	2.1	314957	3	AE003581	AE003581 Drosophila
25	23	2.0	1155	10	AF537215	AF537215 Mus muscu
26	23	2.0	1195	6	AX380404	AX380404 Sequence
27	23	2.0	29865	2	AC020047	AC020047 Drosophila
28	23	2.0	106256	3	AC108135	AC108135 Leishmani
29	23	2.0	124612	2	AC105442	AC105442 Leishmani
30	23	2.0	149964	2	AC120145	AC120145 Mus muscu
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32	23	2.0	167926	3	AC023685	AC023685 Drosophila
33	23	2.0	181510	2	AC120346	AC120346 Mus muscu
34	23	2.0	186030	8	CNS08C7W	AL731747 Oryza sat
35	23	2.0	196900	2	AC020851	AC020851 Mus muscu
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37	22	1.9	646	8	BT005060	BT005060 Arabidops
38	22	1.9	757	8	BT004026	BT004026 Arabidops
39	22	1.9	1200	6	A92047	A92047 Sequence 1
40	22	1.9	1200	6	A92049	A92049 Sequence 3
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# ALIGNMENTS

RESULT 1

AX380398

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

REFERENCE

AUTHORS

TITLE

JOURNAL

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Sequence 3 from Patent WO0200710.

AX380398 GI:19575328

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

REFERENCE

AUTHORS

TITLE

JOURNAL

Patent: WO 0200710-A 3 03-JAN-2002;

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	SLONRSLHGSAYLTQVMGELFIPSVNLVAENECVETCLPSHWTLNLPDIWELGLL	
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	DTGGINIPGVLSLPSLGFSLPTWKGVLGLAGTMLTPTCTLTIRCCCHRRCCGC	
0; Gaps	NCCRCRKRGRFIOFKSEKTKETETESGNENSGYNSDEQKTTDTASLP	
	PKSCSSDEQRNSSCGPPHQADQRP RPASHPQASFNLASPEKVSNTTVV"	
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	1 AGTGATCATGTGGCAGGAGCCATGGAAATAGAGACCCACCGGGTCTGGGTCTGGTAA	
100.0%; Pred. No. 0;	61 TGAAGTCATAGAGGCCCCCAAAATCAAGAGTCCTGAAGGGCTCCAGGCTCGCTTCAA	
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	121 CTGCACCGTCTCCAGGCTGGAAGTCATCATGTGGGCTCTCAGTGACATGTGTGCT	
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	181 AAGCGTCAGGCCCATGAGGCCCATCATCAATGACCGCTTCACTCTCAGAGGTACGA	
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0; Mismatches	481 TCTCTGTGTCAGCCATTCAAGCTATATTTTGTTCGGAGCCAGCCAGCCAGCCAG	
	481 TCTCTGTGTCAGCCATTCAAGCTATATTTTGTTCGGAGCCAGCCAGCCAGCCAG	
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VERSION AX380400.1 GI:19575330  
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ORGANISM Homo sapiens

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AUTHORS Welcher, A., Sarmiento, U.M., Schultze, H.J. and Chute, H.T.  
TITLE B7-like molecules and uses thereof  
JOURNAL Patent: WO 0200710-A 5 03-JAN-2002;  
Amgen, Inc. (US)

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 and Isogai, T.  
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 Isogai, T. and Yamamoto, J.  
 Direct Submission  
 Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7  
 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan  
 (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
 NEDO human cDNA sequencing project supported by Ministry of  
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 Welcher, A.A., Sarmiento, U.M., Schultz, H.J. and Chute, H.T.  
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AUTHORS Taudien,S., Dagand,E., Hildmann,T., Nordsiek,G., Drescher,B., and  
Schatttevoy,R., Weber,J., Schilling,M., Menzel,U., Yaspo,M.L. and  
Rosenthal,A.  
TITLE Direct Submission  
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/note="MZEF, score = 95.1%"
exon
6746..6751
/evidence=not_experimental
/note="GenScan, score = 1.83%, comment = Initial_exon 6 bp
frame: 1 phase: 0"
repeat_region
6901..7339
/evidence=not_experimental
/rpt_family="MLT1C"
7347..7457
/evidence=not_experimental
/rpt_family="LIR16C"
repeat_region
complement(7561..7696)
/evidence=not_experimental
/rpt_family="MIR"
repeat_region
complement(7819..8220)
/evidence=not_experimental
/rpt_family="MLT1J"
exon
8097..8119
/note="GRAIL, score = 45.000%, comment = marginal"
repeat_region
complement(8738..9232)
/evidence=not_experimental
/rpt_family="MLT1C"
exon
complement(9273..9420)
/note="GRAIL, score = 71.000%, comment = good"
exon
9290..9371
/note="GRAIL, score = 81.000%, comment = excellent shadow"
repeat_region
9966..10041
/evidence=not_experimental
/note="homology = 100.00%, score = 38, counts = 2"
/rpt_type=tandem
/rpt_unit="tcttgcacactctctgttgagaggtcggtttatcgc"
repeat_region
10244..10664
/evidence=not_experimental
/rpt_family="MLT1E"
repeat_region
10665..11028
/evidence=not_experimental
/rpt_family="MLT1F"
repeat_region
11318..11417
/evidence=not_experimental
/rpt_family="LIMC/D"
repeat_region
11503..11818
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/rpt_family="AluSg"
exon
complement(11525..11777)
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repeat_region
complement(12346..12827)
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12902..13180
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15255..15299
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exon
16045..16768
/evidence=not_experimental
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/note="GRAIL, score = 54.000%, comment = good"
repeat_region
16823..16850
/evidence=not_experimental
/rpt_family="MER34"
complement(16851..17208)
/evidence=not_experimental
/rpt_family="THEIA"
repeat_region
17209..17632
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/rpt_family="MER34"
complement(17633..17969)
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/rpt_family="AluSg1"
repeat_region
complement(18004..18334)
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/rpt_family="LIR17"
complement(18335..18632)
/evidence=not_experimental
/rpt_family="HERV17"
18352..18420
/note="GRAIL, score = 51.000%, comment = good shadow"
exon
complement(18397..18594)
/note="GRAIL, score = 66.000%, comment = good"
repeat_region
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complement(19228..19361)
/note="MZEF, score = 92.8%"
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20900..21135
/note="MZEF, score = 51.4%"
exon
21150..21275
/evidence=not_experimental
/note="Xpound exon prediction, score = 74% (0%)"

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## Query Match

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Best Local Similarity 27.3%; Score 319; DB 9; Length 142742;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 44 GGTTCCTGGGTCTGTAATGAAGTCATAGAGCCCCCAAAATGCAAGAGTCTCTGAAGGC 103
|||||
Db 44274 GGTTCCTGGGTCTGTAATGAAGTCATAGAGCCCCCAAAATGCAAGAGTCTCTGAAGGC 44333
|||||
QY 104 TCCCAAGGCTCGCTTCAACTGCACCGCTCTCCAGGGCTGGAAGCTCATCATGTGGGCTCTC 163
|||||
Db 44334 TCCCAAGGCTCGCTTCAACTGCACCGCTCTCCAGGGCTGGAAGCTCATCATGTGGGCTCTC 44393
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```

Wed Sep 15 10:41:07 2004

```

164 AGTCACATGTTGGTCTAAGCGTCAGGCCCATGAGCCCATCATCACCAATGACGGCTTC 223
|||||
44394 AGTCACATGTTGGTCTAAGCGTCAGGCCCATGAGCCCATCATCACCAATGACGGCTTC 44453
|||||
224 ACCTCTCAGAGTACGACGAGCGGGGAACCTTACCTCGGAGATGATCATCCACAATGTG 283
|||||
44454 ACCTCTCAGAGTACGACGAGCGGGGAACCTTACCTCGGAGATGATCATCCACAATGTG 44513
|||||
284 GAGCCCACTGATTCCGGGGAACATCATGATGACGCTTCGAGACAGTCGCTGATGATCT 343
|||||
44514 GAGCCCACTGATTCCGGGGAACATCATGATGACGCTTCGAGACAGTCGCTGATGATCT 44573
|||||
344 GCTTACCTTACGTCGACG 362
|||||
44574 GCTTACCTTACGTCGACG 44592
|||||

RESULT 8
HS21C080 340000 bp DNA linear PRI 24-MAY-2000
LOCUS Homo sapiens chromosome 21 segment HS21C080.
DEFINITION AL163280 AP001735 BA000005
ACCESSION AL163280.2 GI:7717369
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 340000)
AUTHORS Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
Park H.S., Toyoda A., Ishii K., Tokoki Y., Choi D.K., Soeda E.,
Chki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
Polley A., Menzel J., Delabar J., Kumpf K., Lehmann R.,
Patterson D., Reichwald K., Rump A., Schilhabel M., Schudy A.,
Zimmermann W., Rosenthal A., Kuch J., Shibuya K., Kawasaki K.,
Asakawa S., Shintani A., Sasaki T., Nagamine K., Mitsuoyama S.,
Antonarakis S.E., Minoshima S., Shimizu N., Nordliek G.,
Hornischer K., Brandt P., Scharfe M., Schoen O., Desario A.,
Reichelt J., Kauer G., Bloeker H., Ranser J., Beck A., Klages S.,
Hennig S., Rieselmann L., Dagand E., Wehrmeyer S., Borzym K.,
Gardiner K., Nizetic D., Francis F., Lehrach H., Reinhardt R. and
Yaspo M.L.
Direct Submission
Submitted (05-MAY-2000) The Chromosome 21 Mapping and Sequencing
Consortium: * RIKEN Genomic Sciences Center, Human Genome Research
Group * Institute of Molecular Biotechnology, Genome Analysis *
Keio University School of Medicine, Dept. of Molecular Biology *
GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular
Genetics (addresses see below)
The Chromosome 21 Mapping and Sequencing Consortium consists of
* RIKEN Genomic Sciences Center, Human Genome Research Group, *
Sagamihara 228-8555, Japan,
* e.mail: sakaki@gsc.riken.go.jp
* URL: http://hgap.gsc.riken.go.jp/
and
* Institute of Molecular Biotechnology, Genome Analysis, *
Butenbergrasse 11, D-07745 Jena, Germany,
* e.mail: gscj-submit@genome.imb-jena.de
* URL: http://genome.imb-jena.de/
and
* Keio University School of Medicine, Dept. of Molecular Biology, *
Tokyo 160-8582, Japan,
* e.mail: shimizu@dnb-med.keio.ac.jp
* URL: http://adenine.dnb.med.keio.ac.jp/
and
* GBF, Dept. of Genome Analysis,
* Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
info.genome@gbf.de
* URL: http://genome.gbf.de/
and
* Max-Planck Institute for Molecular Genetics,
* Innestrasse 73, D-14195 Berlin, Germany,
* e.mail: info-chr21@molgen.mpg.de

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* URL: http://chr21.rz-berlin.mpg.de/.
FEATURES
source
1. 340000
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q22.3"
<1. 125946
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/clone_lib="RPC11,3-5 PAC library"
/note="Accession No. AF121897"
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/chromosome="21"
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/note="Accession No. AF064860"
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/db_xref="taxon:9606"
/chromosome="21"
/map="21q22.3"
/clone="P206A10, 3' partial"
/clone_lib="RPC11,3-5 PAC library"
/note="Accession No. AF121782"
286628..>340000
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/db_xref="taxon:9606"
/chromosome="21"
/map="21q22.3"
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/clone_lib="BAC library"
/note="Accession No. AF064857"
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2398..2495
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/rpt_family="Simple_repeat"
/rpt_type="TANDEM"
complement(2496..2878)
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/rpt_family="LTR/MaLR"
/rpt_type="DISPERSED"
2879..2931
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/rpt_family="Simple_repeat"
/rpt_type="TANDEM"
2932..3004
/note="(TCCA)n"
/rpt_family="Simple_repeat"
/rpt_type="TANDEM"
3005..3074
/note="(TCCA)n"
/rpt_family="Simple_repeat"
/rpt_type="TANDEM"
3473..19157
/gene="SH3BGR"
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/gene="SH3BGR"
join(3473..3565,12649..15426)
CDS

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/ note="Accession No. X93498"
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/ db_xref="GI:7717370"
/ db_xref="GOA:P55822"
/ db_xref="SWISS-PROT:P55822"
/ translation="GSEKAEGETEQAQKEGSEVGNLPEAQKNEEBEGETATERTEE"
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/ number=4
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/ note="L1MD3"
/ rpt_family="LINE/L1"
/ rpt_type=DISPERSED
complement (8482..8762)
/ note="AluJo"
/ rpt_family="SINE/Alu"
/ rpt_type=DISPERSED
complement (8865..8964)
/ note="L2"
/ rpt_family="LINE/L2"
/ rpt_type=DISPERSED
9131..9424
/ note="AluSq"
/ rpt_family="SINE/Alu"
/ rpt_type=DISPERSED
complement (9723..9882)
/ note="L2"
/ rpt_family="LINE/L2"
/ rpt_type=DISPERSED
complement (9989..10077)
/ note="L2"
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/ rpt_type=DISPERSED
complement (10078..10429)
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/ rpt_type=DISPERSED
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10980..11000
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/ rpt_family="Simple_repeat"
/ rpt_type=TANDEM
complement (11002..11282)
/ note="AluSp"
/ rpt_family="SINE/Alu"
/ rpt_type=DISPERSED
complement (11315..11556)
/ note="AluJo"
/ rpt_family="SINE/Alu"
/ rpt_type=DISPERSED
11702..11753
/ note="MIR"
/ rpt_family="SINE/MIR"
/ rpt_type=DISPERSED
12649..12678
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/ number=5
complement (13115..13425)
/ note="AluX"
/ rpt_family="SINE/Alu"
/ rpt_type=DISPERSED
complement (13598..13892)

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Query Match      27.3%; Score 319; DB 9; Length 340000;
Best Local Similarity 100.0%; Pred. No. 3.6e-176;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 GGTTCCTGGGCTCTGGTAATGAACTCATAGAAGCGCCCAAAATGCAAGAGTCTCTGAAGGGC 103
Db 268454 GGTTCCTGGGCTCTGGTAATGAACTCATAGAAGCGCCCAAAATGCAAGAGTCTCTGAAGGGC 268513
QY 104 TCCCAGGCTCGCTTCAACTGCAACCGTCTCCAGGGCTGGAAGCTCATATGTGGGCTCTC 163
Db 268514 TCCCAGGCTCGCTTCAACTGCAACCGTCTCCAGGGCTGGAAGCTCATATGTGGGCTCTC 268573
QY 164 AGTGACATGTGGTCTTAAGGCTAGGGCCATGAGGCCCATCATACCAATGACCGCTTC 223
Db 268574 AGTGACATGTGGTCTTAAGGCTAGGGCCATGAGGCCCATCATACCAATGACCGCTTC 268633
QY 224 ACCTCTCAGAGTACGACCGGGGAACTTCACTCGGAGATGATCATCCAAATGTG 283
Db 268634 ACCTCTCAGAGTACGACCGGGGAACTTCACTCGGAGATGATCATCCAAATGTG 268693
QY 284 GAGCCAGTGTATCGGGAAACATCAGATGCAAGCTCCAGAACAGTCGCGCTCATGGATCT 343
Db 268694 GAGCCAGTGTATCGGGAAACATCAGATGCAAGCTCCAGAACAGTCGCGCTCATGGATCT 268753
QY 344 GCTTACCTTACCGTCCAAG 362
Db 268754 GCTTACCTTACCGTCCAAG 268772

RESULT 9
CH179K04 182532 bp DNA linear PRI 16-OCT-2003
LOCUS Pan troglodytes chromosome 22 BAC CH251-179K04, complete sequence.
DEFINITION AL954228
ACCESSION AL954228
VERSION AL954228.1 GI:37619870
KEYWORDS HTG.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 182532)
The Chimpanzee Chromosome 22 Sequencing Consortium
Chimpanzee chromosome 22 genomic sequence
Unpublished
2 (bases 1 to 182532)
Schafte, M., Berg, C., Conrad, A., Hornischer, K., Loehnert, T.H.,
Ludwig, M., Thies, S., Weber, K. and Bloeker, H.
Direct Submission
Submitted (03-JUN-2003) GBF, Dept. of Genome Analysis, Mascheroder
Weg 1, D-38124 Braunschweig, Germany, E-mail: info.genome@gbf.de
The Chimpanzee Chromosome 22 Sequencing Consortium consists of :
Shanghai, China
Taiwan;
Center: GBF, Braunschweig
Center code: GBF
Web site: http://genome.gbf.de/
Contact: info.genome@gbf.de
----- Project Information
Center project name:
Center clone name: CH251-179K04
----- Summary Statistics
Sequencing vector: ###;
Chemistry: Dye-terminator-amersham: ## of reads
Chemistry: Dye-primer-amersham: ## of reads
Assembly program: ##
Consensus quality: 0 bases at least Q40
Consensus quality: 0 bases at least Q30
Consensus quality: 0 bases at least Q20
Estimated insert size: #: agarose-fp estimation
Estimated insert size: 182532; sum-of-contigs estimation

```

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PROGRAMS AND PARAMETERS USED FOR ANNOTATION:
+ Analysis and annotation were performed with the automatic
+ 'first-pass' annotation and submission tool
+ 'AnnoMitter' (Hornischer & Bloecker)
+ Programs used by 'AnnoMitter':
+
+***** Location/Qualifiers
+*****
+***** 1. 182532
+***** /organism="Pan troglodytes"
+***** /mol_type="genomic DNA"
+***** /db_xref="taxon:9598"
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+***** /clone="CH251-179K04"
+*****
+***** misc_feature
+***** /note="assembly fragment-clone end:T7-vector side:left
+***** assembly_fragment-clone end:SP6-vector side:right"
+*****
+***** ORIGIN
+*****
Query Match 20.6%; Score 241; DB 9; Length 182532;
Best Local Similarity 99.7%; Pred. No. 5.1e-130;
Matches 291; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 361 AGTTATGGAGAGCTCTTCAATCCAGTGTAACTTGTAGTCGCTGAGATGAACCTTG 420
Db 17792 AGTTATGGAGAGCTCTTCAATCCAGTGTAACTTGTAGTCGCTGAGATGAACCTTG 17851

QY 421 TGAAGTACTTGTCTACCTCCACACTGGAGCTGGCTCCGGATATTTCTCGGAGCTCGG 480
Db 17852 TGAAGTACTTGTCTAGCTCAGCTGGAGCTGGCTCCGGATATTTCTCGGAGCTCGG 17911

QY 481 TCTCTCTGGTCAGCATTCAGCTATTAATTTTGTTCGGAGCCAGCAGCTCAAAAGTGC 540
Db 17912 TCTCTCTGGTCAGCATTCAGCTATTAATTTTGTTCGGAGCCAGCAGCTCAAAAGTGC 17971

QY 541 AGTGAGCATCTGGCTGACCCACAGAGCAATGGACCTTGAATTCGCTGGCTACCTG 600
Db 17972 AGTGAGCATCTGGCTGACCCACAGAGCAATGGACCTTGAATTCGCTGGCTACCTG 18031

QY 601 GAAGAGCTCAAGCGCCGCAAGCTGCAACTGTAATCTCACTGTGATTCGG 652
Db 18032 GAAGAGCTCAAGCGCCGCAAGCTGCAACTGTAATCTCACTGTGATTCGG 18083

RESULT 10
LOCUS BS000162 156288 bp DNA linear PRI 07-OCT-2003
DEFINITION Pan troglodytes chromosome 22 clone:PTB-060F12, map 22, complete
sequences.
ACCESSION BS000162
VERSION BS000162.1 GI:37537429
KEYWORDS HTG.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.

REFERENCE 1 The Chimpanzee Chromosome 22 Sequencing Consortium.
AUTHORS DNA sequence of chimpanzee chromosome 22 and its evolutionary
TITLE implications
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 156288)
AUTHORS Saitou,N., Kim,C., Kitano,T., Oota,S., Shimada,M., Kryukov,K.,
TITLE Tomiki,T. and Kohara,Y.
JOURNAL Submitted (15-MAY-2003) Naruya Saitou, National Institute of
Genetics (NIG), Division of Population Genetics, 1111 Yata,
Mishima, Shizuoka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp,
URL:http://sayer.lab.nig.ac.jp/, Tel:81-55-981-6796,
Fax:81-55-981-6789)
COMMENT The Chimpanzee Chromosome 22 Sequencing Consortium consists of:
*Chinese National Human Genome Center at Shanghai, China;

```

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*GBF, Dept. of Genome Analysis, Braunschweig, Germany; *Institute
of Molecular Biotechnology, Jena, Germany; *KRIIBB Genome Research
Center, Daejeon, Korea;
*Max-Planck-Institute for Molecular Genetics, Berlin, Germany;
*National Institute of Genetics, Mishima, Japan;
*National Yang Ming University Genome Research Center, Taipei,
Taiwan;
*RIKEN Genomic Sciences Center, Yokohama, Japan.
----- Genome Center
Center: National Institute of Genetics
Center code: NIG
Web site: http://sayer.lab.nig.ac.jp/
Contact: nsaitou@genes.nig.ac.jp
----- Project Information
Center project name: The Chimpanzee Chromosome 22 Sequencing Project
Center clone name: PTB-060F12
----- Summary Statistics
Sequencing vector: pUC118; 100% of reads
Chemistry: Dye-terminator Big Dye and dGTP; 100% of reads Assembly
Program: Phrap; version 0.990329
Consensus quality: 156,231 bases at least Q40
Consensus quality: 156,288 bases at least Q30
Consensus quality: 156,288 bases at least Q20
-----
This sequence was finished as follows unless otherwise noted: all
regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30);
an attempt was made to resolve all sequencing problems, such as
compressions and repeats; all regions were covered by at one
plasmid
subclone or more than one M13 subclone;
-----
Source information:
The PTB1 chimpanzee BAC library was prepared from DNA isolated from
cultured cells established from the blood of a single male
chimpanzee.
Clones may be obtained from Asao Fujiyama and co-workers
(http://www.gsc.riken.go.jp).
VECTOR: pKS145
-----
Sequence Quality Assessment:
This entry has been annotated with sequence
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in
10,000 bp.
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Neighboring clones: CH251-179K04(left) and PTB-103H04(right).
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FEATURES
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Location/Qualifiers
1. 156288
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/clone="PTB-060F12"
/clone_lib="PTB1 chimpanzee BAC"
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ORIGIN
Query Match 12.4%; Score 145; DB 9; Length 156288;
Best Local Similarity 100.0%; Pred. No. 3.4e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 473 GAGCTCGGTCTCTCTGGTCAGGCATTCAGCTATTAATTTTTCGGAGCCAGCACCTT 532
Db 1 GAGCTCGGTCTCTCTGGTCAGGCATTCAGCTATTAATTTTTCGGAGCCAGCACCTT 60

QY 533 CAAAGTGAGTGAGCATCTCTGCTGCTGCCCCACAGAGCAATGGGACTTTGACTTGCCTG 592
Db 61 CAAAGTGAGTGAGCATCTCTGCTGCTGCCCCACAGAGCAATGGGACTTTGACTTGCCTG 120

QY 593 GCTACTCTGAGAGCTCTGAAGGCC 617

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Db      121  GCTACCTGGAGAGCCTGAGGCC 145

RESULT 11
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LOCUS   AF064857      199665 bp      DNA      linear      PRI 23-JUN-1998
DEFINITION Homo sapiens BAC derived from chromosome 21q22.3, complete
sequence, containing PEP19 (PCP4) gene.
ACCESSION AF064857
VERSION   AF064857.1  GI:3171149
KEYWORDS HTG.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 199665)
AUTHORS   Taudien,S., Nordsiek,G., Korenberg,J., Drescher,B., Weber,J.,
Schatttevoy,R. and Rosenthal,A.
TITLE     Direct Submission
JOURNAL   Submitted (11-MAY-1998) Genome Analysis, Institute for Molecular
Biotechnology, Heutenbergstrasse 11, Jena 07745, Germany
FEATURES
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             747..814
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             complement(1584..2179)
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             2174..3405
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             7781..8020
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Qy	1069	CGACGGGTGATCAACGTC	CCACCGGCGGAGTCA	CCACAGGCTTCTTTAACTCT	1128	
Db	17555	CCAGCGGGTGTATCAACGTC	CCACCGGCGGAGTCA	CCACAGGCTTCTTTAACTCT	17614	
Qy	1129	GGCCAGTCTCTGAGAAGGT	CAGTAAATACACTG	TACTATAG	1168	
Db	17615	GGCCAGTCTCTGAGAAGGT	CAGTAAATACACTG	TACTATAG	17654	

Best Local Similarity	100.0%;	Pred. No. 5.5e-30;			
Matches	72;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
Qy	248	GGGAACCTTCACCTCGAGATGATCATCCACAAATGTGGAGCCCAAGTATTTCGGGGAAACATC	307		
Db	191622	GGGAACCTTCACCTCGAGATGATCATCCACAAATGTGGAGCCCAAGTATTTCGGGGAAACATC	191681		
Qy	308	AGATGCAGCCTC	319		
Db	191682	AGATGCAGCCTC	191693		
RESULT 13					
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LOCUS					
DEFINITION	AF064860	170121 bp	DNA	linear	PRI 05-MAR-2002
ACCESSION	AF064860	2	GI:18958624		
VERSION	HTG; HTGS_DRAFT				
KEYWORDS	HTG; HTGS_DRAFT				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
	1 (bases 1 to 170121)				
	Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,				
	Park,H.-S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.-K., Soeda,E.,				
	Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,				
	Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,				
	Patterson,D., Reichwald,K., Rump,A., Schillhabel,M.B., Schudy,A.,				
	Zimmermann,W., Rosenthal,A., Kudoh,J., Kawasaki,K., Asakawa,S.,				
	Shintani,A., Sasaki,T., Nagamine,K., Mitsuyama,S.,				
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	Hornischer,K., Brandt,P., Scharfe,M., Schoen,O., Desario,A.,				
	Reichelt,J., Kauer,G., Bloecker,H., Ramser,J., Beck,A., Klages,S.,				
	Hennig,S., Riesselmann,L., Degand,E., Haaf,F., Wehrmeyer,S.,				
	Borzym,K., Gardiner,K., Nizetic,D., Francis,F., Lehrach,H.,				
	Reinhardt,R. and Yaspo,M.Laure.				
TITLE	The DNA sequence of human chromosome 21				
JOURNAL	Nature 405 (6784), 311-319 (2000)				
MEDLINE	Nature 405 (6784), 311-319 (2000)				
PUBMED	10830953				
REFERENCE	2 (bases 1 to 170121)				
AUTHORS	Rump,A., Degand,E., Hildmann,T., Nordsiek,G., Drescher,B.,				
	Weber,J., Schattevoy,R., Yaspo,M.-L. and Rosenthal,A.				
TITLE	Direct Submission				
JOURNAL	Submitted (12-MAY-1998) Genome Analysis, Institute of Molecular				
	Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany				
REFERENCE	3 (bases 1 to 170121)				
AUTHORS	Rump,A., Degand,E., Hildmann,T., Nordsiek,G., Drescher,B.,				
	Weber,J., Schattevoy,R., Yaspo,M.-L., Rosenthal,A.,				
	Rosenthal,A.				
TITLE	Direct Submission				
JOURNAL	Submitted (27-FEB-2002) Genome Analysis, Institute of Molecular				
	Biotechnology, Beutenbergstr. 11, Jena 07745, Germany				
REFERENCE	4 (bases 1 to 170121)				
AUTHORS	Rump,A., Degand,E., Hildmann,T., Nordsiek,G., Drescher,B.,				
	Weber,J., Schattevoy,R., Yaspo,M.-L. and Rosenthal,A.				
TITLE	Direct Submission				
JOURNAL	Submitted (05-MAR-2002) Genome Analysis, Institute of Molecular				
	Biotechnology, Beutenbergstr. 11, Jena 07745, Germany				
COMMENT	On Feb 27, 2002 this sequence version replaced gi:3171153.				
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.031;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 840 GCTGCTGCCGTTGTTCTTCTGCTG 864  
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Db 1574 GCTGCTGCCGTTGTTCTTCTGCTG 1550

RESULT 15

AY119603 5178 bp mRNA linear INV 15-JUN-2002  
Drosophila melanogaster LD27161 full insert cDNA.  
ACCESSION AV119603  
VERSION AV119603.1 GI:21429075  
KEYWORDS FLI cDNA  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 5178)  
Scapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,  
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,  
George, R., Gonzalez, M., Guarini, H., Kronmiller, B., Li, P., Liao, G.,  
Miranda, A., Mungall, C. J., Nunco, J., Pacleb, J., Paragas, V., Park, S.,  
Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Rubin, G. M.  
and Celniker, S.

Direct Submission  
Submitted (10-JUN-2002) Berkeley Drosophila Genome Project,  
Lawrence Berkeley National Laboratory, One Cyclotron Road,  
Berkeley, CA 94720, USA  
Sequence submitted by:  
Berkeley Drosophila Genome Project  
Lawrence Berkeley National Laboratory  
Berkeley, CA 94720

This clone was sequenced as part of a high-throughput process to  
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,  
Science 2000). The sequence has been subjected to integrity checks  
for sequence accuracy, presence of a polyA tail and contiguity  
within 100 kb in the genome. Thus we believe the sequence to  
reflect accurately this particular cDNA clone. However, there are  
artifacts associated with the generation of cDNA clones that may  
have not been detected in our initial analyses such as internal  
priming, priming from contaminating genomic DNA, retained introns  
due to reverse transcription of unspliced precursor RNAs, and  
reverse transcriptase errors that result in single base changes.  
For further information about this sequence, please visit our location  
and relationship to other sequences, please visit our Web site  
(http://fruitfly.berkeley.edu) or send email to  
cdna@fruitfly.berkeley.edu.

FEATURES

source

1. 5178  
Location/Qualifiers  
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/mol\_type="mRNA"  
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CDS

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ORIGIN

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 800 CGCTGCTGCTGCTGCCGCGCTCGT 823  
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Db 216 CGCTGCTGCTGCTGCCGCGCTCGT 193

Search completed: September 15, 2004, 03:47:23  
Job time : 4803.11 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 19:19:38 ; Search time 501.037 Seconds  
(without alignments)  
9903.249 Million cell updates/sec

**Title:** US-09-729-264-3

Perfect score:

Sequence: 1 agtgatcatgtgtggcaggag.....gtaatacaactgtagtatag 1168

Scoring table: OLIGO NUC

CGIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 16

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N Geneset 29Jan04:\*

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1: geneseqn1980as:*
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10: geneseqn2004as:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Query %	Length	DB	ID	Description
1	1168	100.0	1168	6	ABK13029	Abk13029	DNA encod
2	1027	87.9	1175	6	ABK13028	Abk13028	DNA encod
3	976	83.6	1240	6	ABK13030	Abk13030	DNA encod
4	976	83.6	2051	9	ADB62950	ADB62950	Human cDN
5	771	66.0	1139	6	ABK13031	Abk13031	DNA encod
6	677	58.0	1392	5	AAS922356	AAS922356	DNA encod
7	217	18.6	474	8	ACH16130	Ach16130	Human adu
8	191	16.4	401	4	AAI36582	Aai36582	Probe #52
9	25	2.1	357	5	AAJ04335	Aai04335	Probe #43
10	24	2.1	6507	4	ABU15493	Abu15493	Drosophil
11	24	2.1	5967	4	ABU15492	Abu15492	Drosophil
12	23	2.0	1195	6	ABK13032	Abk13032	DNA encod
13	22	1.9	141	2	AAV99359	Aav99359	5' PCR pr
14	22	1.9	767	6	ABN99162	Abn99162	Arabidops
15	22	1.9	1200	2	AAV35364	Aav35364	Human GDN
16	22	1.9	1200	2	AAV35365	Aav35365	Human GDN
17	22	1.9	1203	3	AAAI2547	AAAI2547	DNA encod
18	22	1.9	1699	2	AAV00251	Aav00251	Human Ret
19	22	1.9	1792	3	AAZ29104	Aaz29104	Human GFR
20	22	1.9	1809	2	AAV99333	Aav99333	Glia1 cel
21	22	1.9	1829	3	AAZ93702	Aaz93702	PRO538 DN
22	22	1.9	1829	3	AAH89519	Aah89519	Human PRO
23	22	1.9	1829	3	AAA77617	Aaa77617	Human PRO

Claim 1; Fig 2; 135pp; English.

PS The invention relates to an isolated B7-like (B7-L) polypeptide (I). The  
XX polypeptide, polynucleotide encoding it and antibody against (I) are  
CC useful for treating B7-like polypeptide-related disease, disorders or  
CC conditions including reproductive disorders (e.g. infertility,  
CC miscarriage, preterm labour and delivery and endometriosis) and  
CC proliferative disorders. Antibodies, soluble proteins comprising  
CC extracellular domains and other regulators of B7-L polypeptides are  
CC useful for enhancing the immune response to tumours. (I) plays a role in  
CC growth and maintenance of cancer cells based on the observation of  
CC seminal vesicle hyperplasia in transgenic mice overexpressing B7-L  
CC polypeptide. Hence modulators of (I) are useful for the treatment of  
CC cancer including seminal vesicle cancer, lung, brain, breast, ovarian,  
CC testicular cancer and cancers of haematopoietic system. B7-L polypeptide  
CC pathway can be manipulated to regulate cytotoxic T-lymphocyte response in  
CC allograft transplantation, graft versus host disease, T-cell dependent B-  
CC cell mediated diseases and autoimmune diseases. B7-L molecules are useful  
CC for alleviating the symptoms associated with diseases involving chronic  
CC immune cell dysfunction or to treat autoimmune diseases such as systemic  
CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes,  
CC immune thrombocytopenic purpura and psoriasis, chronic inflammatory  
CC disease such as inflammatory bowel disease (Crohn's disease and  
CC ulcerative colitis). Grave's disease, Hashimoto's thyroiditis and  
CC diabetes mellitus. They are also useful as immunosuppressive agents for  
CC bone marrow and organ transplantation or to prolong graft survival. B7-L  
CC molecules are also useful for diagnosis and treatment of diseases  
CC involving abnormal cell proliferation, including arteriosclerosis and  
CC vascular restenosis. Antagonists of B7-L polypeptides are useful for  
CC alleviation of toxic shock syndrome or all sensitisation due to blood  
CC transfusions, and for treatment of allergy, asthma and hypersensitivity  
CC reactions, nephropathies (e.g. glomerulonephritis), skin disorders  
CC (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various  
CC pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease,  
CC anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia  
CC gravis, and lymphoproliferative disorders such as multiple myeloma. The  
XX present sequence represents the coding sequence of human B7-L\_h2

SQ Sequence 1168 BP; 299 A; 302 C; 288 G; 279 T; 0 U; 0 Other;

Query Match		100.0%;	Score 1168;	DB 6;	Length 1168;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1168;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AGTGATCATGTGCGAGGAGCCATCGAAGAAATAGAGACCCCGGTTCTGGTCTGGTAA	60		
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QY	61	TGAAGTCATAGAGGCCCCCAAAATGCAAGAGTCTGAAGGCTCCAGGCTCGCTTCAA	120		
DB	61	TGAAGTCATAGAGGCCCCCAAAATGCAAGAGTCTGAAGGCTCCAGGCTCGCTTCAA	120		
QY	121	CTGCACCGCTCTCCAGGAGCTGGAAGCTCATCATGTGGGCTCTCAGTGACATGGTGGTCT	180		
DB	121	CTGCACCGCTCTCCAGGAGCTGGAAGCTCATCATGTGGGCTCTCAGTGACATGGTGGTCT	180		
QY	181	AGCGTCAGGCGCCATGAGGAGCCCATCATCAATGACCGCTTCACTCTCAGAGTACGA	240		
DB	181	AGCGTCAGGCGCCATGAGGAGCCCATCATCAATGACCGCTTCACTCTCAGAGTACGA	240		
QY	241	CCAGGCGGGAATCTCACTCCGAGATGATCATCAATGTGGAGCCGAGTATTCTGGG	300		
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QY	301	GAAATCATGATGAGGCTCCAGAACAGTCCGCTGCATGATCTGCTTACCTTACCGTCA	360		
DB	301	GAAATCATGATGAGGCTCCAGAACAGTCCGCTGCATGATCTGCTTACCTTACCGTCA	360		
QY	361	AGTTATGGAGAGCTGTTATTCCTCCAGTGTATCTGTAGTCGTGAGAAATCAACTTG	420		
DB	361	AGTTATGGAGAGCTGTTATTCCTCCAGTGTATCTGTAGTCGTGAGAAATCAACTTG	420		
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DB	421	TGAAGTTACTTGTCTACCTCACACTGGAGCTGGCTCCCGGATATTTCTGGAGCTCGG	480		
QY	481	TCTCTGTCTAGCCATTCAAGCTATTATTTGTTCCGGAGCCAGGACCTTCAAGTGC	540		
DB	481	TCTCTGTCTAGCCATTCAAGCTATTATTTGTTCCGGAGCCAGGACCTTCAAGTGC	540		
QY	541	AGTGAGCATCTCGGCTCTGACCCACAGCAATGGGACTTTGACTTGGTGGCTACCTG	600		
DB	541	AGTGAGCATCTCGGCTCTGACCCACAGCAATGGGACTTTGACTTGGTGGCTACCTG	600		
QY	601	GAAGAGCTGAGGCCCCGCAAGTCTGCAACTGTAAATCTCACTGTGATTCGCTGCCCA	660		
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QY	781	GAGCTGTACTCTTACAAATACGCTGCTGCTGCCCGCTGCTTGTGTGGCTGCAACTG	840		
DB	781	GAGCTGTACTCTTACAAATACGCTGCTGCTGCCCGCTGCTTGTGTGGCTGCAACTG	840		
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DB	961	CGGCTCAATTCAGATCAACAAAGAGCAACAGACACCGCTTCTCTCCCTCCAAATCTG	1020		
QY	1021	TGAATCCAGTGTATCTGAAACAAAGAGCAACAGTGTGGGCTCTCCACAGCGGCTGA	1080		
DB	1021	TGAATCCAGTGTATCTGAAACAAAGAGCAACAGTGTGGGCTCTCCACAGCGGCTGA	1080		
QY	1081	TCAAGTCCACCGAGGCGCAAGTCTCCACAGGCTTCTTTTAACTTGGCCAGTCTGA	1140		
DB	1081	TCAAGTCCACCGAGGCGCAAGTCTCCACAGGCTTCTTTTAACTTGGCCAGTCTGA	1140		
QY	1141	GAAAGTCAGTAATACAACTGTAGTATAG	1168		
DB	1141	GAAAGTCAGTAATACAACTGTAGTATAG	1168		

RESULT 2

ABK13028 standard; cDNA; 1175 BP.

ID ABK13028

AC ABK13028;

DT 23-APR-2002 (first entry)

DE DNA encoding human B7-like protein, B7-L\_h1.

Human; B7-like protein; B7-L; anti-infectivity; gynaecological;  
antitumour; cytostatic; immunosuppressive; antiarthritic; antineoplastic;  
antiinflammatory; dermatological; antipsoriatic; neuroprotective;  
antidiabetic; haemostatic; antithyroid; antitumor; antiallergic;  
antidiabetic; nephrotropic; antibacterial; virucide; tumour; cancer;  
reproductive disorder; graft versus host disease; autoimmune disease;  
toxic shock syndrome; allergy; nephropathy; skin disorder;  
endocrinopathy; lymphoproliferative disorder; gene; ss.

Homo sapiens.

XX



PH	Key	Location/Qualifiers	
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FT		/*tag= a	
FT		/product= "B7-like protein, B7-L_h1"	
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PN	WO200200710-A2.		
PD	03-JAN-2002.		
XX			
PF	28-JUN-2001; 2001WO-US020719.		
XX			
PR	28-JUN-2000; 2000US-0214512P.		
PR	28-NOV-2000; 2000US-00729264.		
XX			
PA	(ANGE-) AMGEN INC.		
XX			
PI	Welcher AA, Sarmiento UM, Schultz HJ, Chute HT;		
XX			
DR	WPI; 2002-130881/17.		
DR	P-PSDB; AAU75540.		
XX			
PT	New B7-like polypeptides, polynucleotides and their modulators, useful		
PT	for diagnosing, preventing and treating reproductive, immune and		
PT	proliferative disorders, e.g. cancer and arteriosclerosis.		
XX			
PS	Claim 1; Fig 1; 135pp; English.		
XX			
CC	The invention relates to an isolated B7-like (B7-L) polypeptide (I). The		
CC	polypeptide, polynucleotide encoding it and antibody against (I). The		
CC	useful for treating B7-like polypeptide-related disease, disorders or		
CC	conditions including reproductive disorders (e.g. infertility,		
CC	miscarriage, preterm labour and delivery and endometriosis) and		
CC	proliferative disorders. Antibodies, soluble proteins comprising		
CC	extracellular domains and other regulators of B7-L polypeptides are		
CC	useful for enhancing the immune response to tumours. (I) plays a role in		
CC	growth and maintenance of cancer cells based on the observation of		
CC	seminal vesicle hyperplasia in transgenic mice overexpressing B7-L		
CC	polypeptide. Hence modulators of (I) are useful for the treatment of		
CC	cancer including seminal vesicle cancer, lung, brain, breast, ovarian,		
CC	testicular cancer and cancers of haematopoietic system. B7-L polypeptide		
CC	pathway can be manipulated to regulate cytotoxic T-lymphocyte response in		
CC	allograft transplantation, graft versus host disease, T-cell dependent B-		
CC	cell mediated diseases and autoimmune diseases. B7-L molecules are useful		
CC	for alleviating the symptoms associated with diseases involving chronic		
CC	immune cell dysfunction or to treat autoimmune diseases such as systemic		
CC	lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes,		
CC	immune thrombocytopenic purpura and psoriasis, chronic inflammatory		
CC	disease such as inflammatory bowel disease (Crohn's disease and		
CC	ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and		
CC	diabetes mellitus. They are also useful as immunosuppressive agents for		
CC	bone marrow and organ transplantation or to prolong graft survival. B7-L		
CC	molecules are also useful for diagnosis and treatment of diseases		
CC	involving abnormal cell proliferation, including arteriosclerosis and		
CC	vascular stenosis. Antagonists of B7-L polypeptides are useful for		
CC	alleviation of toxic shock syndrome or allosensitisation due to blood		
CC	transfusions, and for treatment of allergy, asthma and hypersensitivity		
CC	reactions, nephropathies (e.g. glomerulonephritis), skin disorders		
CC	(pemphigus and pemphigoid), endocrinopathies (Grave's disease), various		
CC	pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease,		
CC	anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia		
CC	gravis, and lymphoproliferative disorders such as multiple myeloma. The		
CC	present sequence represents the coding sequence of human B7-L_h1		
XX			
SQ	Sequence 1175 BP; 295 A; 307 C; 286 G; 287 T; 0 U; 0 Other;		
	Query Match	87.9%; Score 1027; DB 6; Length 1175;	
	Best Local Similarity	99.9%; Pred. No. 0;	
	Matches 1077; Conservative	0; Mismatches	1; Indels
		0; Gaps	0;
QY	91 AGTCCTGAAGGGCTCCAGGCTCGCTTCAACTGCACCGCTCCAGGGCTGGAAGCTCAT	150	
DB	98 AGTCCTGAAGGGCTCCAGGCTCGCTTCAACTGCACCGCTCCAGGGCTGGAAGCTCAT	157	

QY	151	CATGTGGGCTCTCAGTGACATGGTGGTCTTAAGCGCTCAGGCCCATGAGCCCATCATCAC	210
DB	158	CATGTGGGCTCTCAGTGACATGGTGGTCTTAAGCGCTCAGGCCCATGAGCCCATCATCAC	217
QY	211	CAATGACCGCTTCACTCTCAGAGGTACGACACAGGGCGGGAACCTTCCACTCCGAGATGAT	270
DB	218	CAATGACCGCTTCACTCTCAGAGGTACGACACAGGGCGGGAACCTTCCACTCCGAGATGAT	277
QY	271	CATCCACAATGTGGAGCCCATGATTTGGGGAACATCAGATGCGACCTCCAGAACAGTCG	330
DB	278	CATCCACAATGTGGAGCCCATGATTTGGGGAACATCAGATGCGACCTCCAGAACAGTCG	337
QY	331	CCTGCATGATCTGCTTACCTTACCGTCCAAAGTTATGGAGAGCTGTTCAATCCAGTGT	390
DB	338	CCTGCATGATCTGCTTACCTTACCGTCCAAAGTTATGGAGAGCTGTTCAATCCAGTGT	397
QY	391	TAATCTTTGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCTCAGCTGAC	450
DB	398	TAATCTTTGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCTCAGCTGAC	457
QY	451	CTGCTCCCGGATATTTCTGGGAGTCGGTCTCTCGTCAAGCATTCAAGCTATTATT	510
DB	458	CCGCTCCCGGATATTTCTGGGAGTCGGTCTCTCGTCAAGCATTCAAGCTATTATT	517
QY	511	TGTTCCGGAGCCGACGACCTTCAAGTCAGTGAGCATCTGCTCTGACCCACAGAG	570
DB	518	TGTTCCGGAGCCGACGACCTTCAAGTCAGTGAGCATCTGCTCTGACCCACAGAG	577
QY	571	CAATGGGACTTTGACTTTGGTGGCTACCTCGAAGAGCTCGAAGCCCGCAAGTCTGCAAC	630
DB	578	CAATGGGACTTTGACTTTGGTGGCTACCTCGAAGAGCTCGAAGCCCGCAAGTCTGCAAC	637
QY	631	TGTAAATCTCAGTGTGATTCGGTGTCCCAAGACACTGGAGGTGGTATTATATTCAGG	690
DB	638	TGTAAATCTCAGTGTGATTCGGTGTCCCAAGACACTGGAGGTGGTATTATATTCAGG	697
QY	691	TGTATTATCAAGTTTACCGAGTTTAGTGTTCCTTTCATTCGCTTACTTGGGGCAAGTGGACT	750
DB	698	TGTATTATCAAGTTTACCGAGTTTAGTGTTCCTTTCATTCGCTTACTTGGGGCAAGTGGACT	757
QY	751	TGGACTTAGCAGGCACCATGCTTCTGACGGCGAGCTGTACTTCTTACAATACGCTGCTGCTG	810
DB	758	TGGACTTAGCAGGCACCATGCTTCTGACGGCGAGCTGTACTTCTTACAATACGCTGCTGCTG	817
QY	811	CTGCCCGCTGCTGTTGTTGGCTGMAACTGCTGCTCCCGTGTGTTTCTGCTGTAGAAG	870
DB	818	CTGCCCGCTGCTGTTGTTGGCTGMAACTGCTGCTCCCGTGTGTTTCTGCTGTAGAAG	877
QY	871	AAAAAGAGGATTTGCTGATTTCAATTTCAAAGAAATCTGAAAGAAATGAAAGAAAGAAAGAA	930
DB	878	AAAAAGAGGATTTGCTGATTTCAATTTCAAAGAAATCTGAAAGAAATGAAAGAAAGAAAGAA	937
QY	931	AACCTGAGACAGAAAGTGGAAATGAAATCTCCGCTACAAATTCAGATGAACAAAGAACAC	990
DB	938	AACCTGAGACAGAAAGTGGAAATGAAATCTCCGCTACAAATTCAGATGAACAAAGAACAC	997
QY	991	AGACACCGCTTCTCTCCCTCCCAATCTGTAATCCAGTGTGATTCAGTGAACAAAGAAACAG	1050
DB	998	AGACACCGCTTCTCTCCCTCCCAATCTGTAATCCAGTGTGATTCAGTGAACAAAGAAACAG	1057
QY	1051	TAGCTGTGGCCCTCTCACCAGCGGGCTGATCAAGTCCACCAGGCGCAGCAAGTCATCC	1110
DB	1058	TAGCTGTGGCCCTCTCACCAGCGGGCTGATCAAGTCCACCAGGCGCAGCAAGTCATCC	1117
QY	1111	ACAGGCTTCTTTTAAATCTGGCCAGTCTCTGAGAAGTCTAGTAATCAACTGTAGTATAG	1168
DB	1118	ACAGGCTTCTTTTAAATCTGGCCAGTCTCTGAGAAGTCTAGTAATCAACTGTAGTATAG	1175

RESULT 3  
ABK13030  
ID ABK13030 standard; cDNA; 1240 BP.  
XX

Wed Sep 15 10:41:07 2004

ABK13030;  
23-APR-2002 (first entry)  
DNA encoding human B7-like protein, B7-L\_h3.  
Human; B7-like protein; B7-L; antinfertility; gynaecological;  
antitumor; cytostatic; immunosuppressive; antiarthritic; antirheumatic;  
antiinflammatory; dermatological; antiporiatic; neuroprotective;  
antidiabetic; haemostatic; antithyroid; antitumor; antiallergic;  
antiasthmatic; nephrotropic; antibacterial; virucide; tumor; cancer;  
reproductive disorder; graft versus host disease; autoimmune disease;  
toxic shock syndrome; allergy; nephropathy; skin disorder;  
endocrinopathy; lymphoproliferative disorder; gene; ss.  
Homo sapiens.  
OS  
XX  
XX  
KW Key Location/Qualifiers  
FH CDS 80..1240  
FT /\*tag= a  
FT /product= "B7-like protein, B7-L\_h3"  
XX  
XX  
PN WO200200710-A2.  
XX  
XX 03-JAN-2002.  
XX 28-JUN-2001; 2001WO-US020719.  
XX 28-JUN-2000; 2000US-0214512P.  
XX 28-NOV-2000; 2000US-00729264.  
XX (AMGE-) AMGEN INC.  
XX  
XX Welcher AA, Sarmiento UM, Schultz HJ, Chute HT;  
PI WPI; 2002-130881/17.  
XX P-PSDB; AAU75542.  
XX  
XX New B7-like polypeptides, polynucleotides and their modulators, useful  
PT for diagnosing, preventing and treating reproductive, immune and  
PT proliferative disorders, e.g. cancer and arteriosclerosis.  
XX  
XX Claim 1; Fig 3; 135pp; English.  
XX  
XX The invention relates to an isolated B7-like (B7-L) polypeptide (I). The  
CC polypeptide, polynucleotide encoding it and antibody against (I) are  
CC useful for treating B7-like polypeptide-related disease, disorders or  
CC conditions including reproductive disorders (e.g. infertility,  
CC miscarriage, preterm labour and delivery and endometriosis) and  
CC proliferative disorders. Antibodies, soluble proteins comprising  
CC extracellular domains and other regulators of B7-L polypeptides are  
CC useful for enhancing the immune response to tumours. (I) plays a role in  
CC growth and maintenance of cancer cells based on the observation of  
CC seminal vesicle hyperplasia in transgenic mice overexpressing B7-L  
CC polypeptide. Hence modulators of (I) are useful for the treatment of  
CC cancer including seminal vesicle cancer, lung, brain, breast, ovarian,  
CC testicular cancer and cancers of haematopoietic system. B7-L polypeptide  
CC pathway can be manipulated to regulate cytotoxic T-lymphocyte response in  
CC allograft transplantation, graft versus host disease, T-cell dependent B-  
CC cell mediated diseases and autoimmune diseases. B7-L molecules are useful  
CC for alleviating the symptoms associated with diseases involving chronic  
CC immune cell dysfunction or to treat autoimmune diseases such as systemic  
CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes,  
CC immune thrombocytopenic purpura and psoriasis, chronic inflammatory  
CC disease such as inflammatory bowel disease (Crohn's disease and  
CC ulcerative colitis). Grave's disease, Hashimoto's thyroiditis and  
CC diabetes mellitus. They are also useful as immunosuppressive agents for  
CC bone marrow and organ transplantation or to prolong graft survival. B7-L  
CC molecules are also useful for diagnosis and treatment of diseases  
CC involving abnormal cell proliferation, including arteriosclerosis and  
CC vascular restenosis. Antagonists of B7-L polypeptides are useful for  
CC alleviation of toxic shock syndrome or allosensitisation due to blood  
CC transfusions, and for treatment of allergy, asthma and hypersensitivity

CC reactions, nephropathies (e.g. glomerulonephritis), skin disorders  
CC (pemphigus and pemphigoid), endorinopathies (Grave's disease), various  
CC pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease,  
CC anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia  
CC gravis, and lymphoproliferative disorders such as multiple myeloma. The  
CC present sequence represents the coding sequence of human B7-L\_h3  
SQ Sequence 1240 BP; 318 A; 319 C; 305 G; 298 T; 0 U; 0 Other;  
Query Match 83.6%; Score 976; DB 6; Length 1240;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1076; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 91 AGTCTCTGAAGGCTCCAGGCTCGCTTCAACTGACCGCTCTCCAGGGCTGAAGCTCAT 150  
DB 163 AGTCTCTGAAGGCTCCAGGCTCGCTTCAACTGACCGCTCTCCAGGGCTGAAGCTCAT 222  
QY 151 CATGTGGGCTCTCAGTGACATGGTGTCTAGCGCTCAGGCGCATGGAGCCCATCATCAC 210  
DB 223 CATGTGGGCTCTCAGTGACATGGTGTCTAGCGCTCAGGCGCATGGAGCCCATCATCAC 282  
QY 211 CAATGACCGCTTCACTCTCAGAGGTACGACGAGGCGGGAACTTCACCTCGGAGATGAT 270  
DB 283 CAATGACCGCTTCACTCTCAGAGGTACGACGAGGCGGGAACTTCACCTCGGAGATGAT 342  
QY 271 CATCCAATGTGGAGCCAGTGATTCGGGGAAACATCAGATGAGGCTCCAGAACAGTCG 330  
DB 343 CATCCAATGTGGAGCCAGTGATTCGGGGAAACATCAGATGAGGCTCCAGAACAGTCG 402  
QY 331 CCTGCATGATCTGCTTACCTTACCGTCAAGTTATGGGAGAGCTGTTTCAATCCCAAGTGT 390  
DB 403 CCTGCATGATCTGCTTACCTTACCGTCAAGTTATGGGAGAGCTGTTTCAATCCCAAGTGT 462  
QY 391 TAACTTTGTAGTCGCTGAGAACTGAACTTGTGAAGTTACTTGTCTACCTCCACATCGGAC 450  
DB 463 TAACTTTGTAGTCGCTGAGAACTGAACTTGTGAAGTTACTTGTCTACCTCCACATCGGAC 522  
QY 451 CTGGCTCCCGGATATTTCTGGGAGCTCGGTCTCTCTGCTCAGCATTCAGAGCTATTATTT 510  
DB 523 CCGGCTCCCGGATATTTCTGGGAGCTCGGTCTCTCTGCTCAGCATTCAGAGCTATTATTT 582  
QY 511 TGTTCGGAGCCAGGAGCCCTTCAAAGTCAGTGAGCATCTTGGCTCTGACCCACACAGAG 570  
DB 583 TGTTCGGAGCCAGGAGCCCTTCAAAGTCAGTGAGCATCTTGGCTCTGACCCACACAGAG 642  
QY 571 CAATGGGACTTTGACTTTGCTGGCTACCTGGAAGAGCTGGAAGCCCGGAGTCTGCAAC 630  
DB 643 CAATGGGACTTTGACTTTGCTGGCTACCTGGAAGAGCTGGAAGCCCGGAGTCTGCAAC 702  
QY 631 TGTAAATCTCAGTGTGATTCGCTCCCGAGACACTGGAGTGTATTAATATTTCCAGG 690  
DB 703 TGTAAATCTCAGTGTGATTCGCTCCCGAGACACTGGAGTGTATTAATATTTCCAGG 762  
QY 691 TGTAAATCTCAGTGTGATTCGCTCCCGAGACACTGGAGTGTATTAATATTTCCAGG 750  
DB 763 TGTAAATCTCAGTGTGATTCGCTCCCGAGACACTGGAGTGTATTAATATTTCCAGG 822  
QY 751 TGGACTAGCAGGACCATGCTTCTGACGCGGAGTGTACTCTTACAATACGCTGCTG 810  
DB 823 TGGACTAGCAGGACCATGCTTCTGACGCGGAGTGTACTCTTACAATACGCTGCTG 882  
QY 811 CTGCGCGCTGCTGTTGTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 870  
DB 883 CTGCGCGCTGCTGTTGTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 942  
QY 871 AAAAGAGGATTTCTGATTTCAATTTCAAAAGAAATCTGAAAAGAGAGAGACAAAGAGA 930  
DB 943 AAAAGAGGATTTCTGATTTCAATTTCAAAAGAAATCTGAAAAGAGAGAGACAAAGAGA 1002  
QY 931 AACTCAGACAGAAAGTGAATGAAAATTCGGGCTACAAATTCAGATGACAAAGAGCCAC 990  
DB 1003 AACTCAGACAGAAAGTGAATGAAAATTCGGGCTACAAATTCAGATGACAAAGAGCCAC 1062

QY 991 AGACACCGCTTCTCTCCCTCCCAATCTCTGTGAATCCAGTATCTCTGAAACAAGAACAG 1050  
 Db |||||  
 1063 AGAAACCGCTTCTCTCCCTCCCAATCTCTGTGAATCCAGTATCTCTGAAACAAGAACAG 1122  
 QY 1051 TAGCTGTGGCCCTCTCTACACAGCGGCTGATCAACAGTCCACCCAGCCAGCAAGTCATCC 1110  
 Db |||||  
 1123 TAGCTGTGGCCCTCTCTACACAGCGGCTGATCAACAGTCCACCCAGCCAGCAAGTCATCC 1182  
 QY 1111 ACAGGCTCTTTTAATCTGGCCAGTCTCTGAGAGGTCTAGTATCAAACTGTAGTATAG 1168  
 Db |||||  
 1183 ACAGGCTCTTTTAATCTGGCCAGTCTCTGAGAGGTCTAGTATCAAACTGTAGTATAG 1240

## RESULT 4

ADB62950

ID ADB62950 standard; cDNA; 2051 BP.

AC ADB62950;

XX 04-DEC-2003 (first entry)

XX Human cDNA encoding clone PLACE60177880.

XX Human; ss; Gene; pharmaceutical; diagnostic; gene therapy;  
 KW tissue regeneration; cell regeneration; membrane protein;  
 KW signal transduction-related protein; transcription-related protein;  
 KW osteoporosis; neurological disease; cancer; tumour.

XX Homo sapiens.

XX Key Location/Qualifiers

FH 104..1327

FT /\*tag= a

FT /product= "Clone PLACE60177880 protein"

XX EP1308459-A2.

XX 07-MAY-2003.

XX 28-MAR-2002; 2002EP-00007401.

XX 05-NOV-2001; 2001JP-00379298.

PR 25-JAN-2002; 2002US-00350978.

XX (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Tamechika I;

PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX

DR WPI; 2003-450961/43.

DR P-FSDB; ADB64920.

XX

PT New polynucleotides and polypeptides, useful for developing a diagnostic  
 PT marker or medicines for regulation of their expression and activity, or  
 PT as targets of gene therapy.

XX

PS Claim 1; Page; 222pp; English.

XX

CC The invention discloses a polynucleotide comprising a sequence selected  
 CC from 1970 fully defined nucleotide sequences which encode novel  
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide  
 CC or its partial peptide, an antibody binding to the polypeptide or peptide  
 CC of the polynucleotide, immunologically assaying the polypeptide or  
 CC peptide of the polynucleotide by contacting the polypeptide or  
 CC with the antibody of the encoded protein, and observing the binding  
 CC between the two, a transformant carrying the polynucleotide in an  
 CC expressible manner and an antisense polynucleotide. The oligonucleotide  
 CC is useful as a primer for synthesising the polynucleotide, or as a probe  
 CC for detecting the polynucleotide. The polynucleotides and encoded  
 CC proteins are useful as pharmaceutical agents and many disease-related  
 CC genes may be included in them, for developing a diagnostic marker or

CC medicines for regulation of their expression and activity, or as targets  
 CC of gene therapy. The genes are involved in tissue and/or cell  
 CC regeneration. Membrane proteins, signal transduction-related genes,  
 CC transcription-related proteins, disease-related proteins and genes  
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,  
 CC neurological diseases, cancer, tumours). The cDNA may be used to regulate  
 CC the activity or expression of the encoded protein to treat diseases. The  
 CC sequence presented is a cDNA of the invention. Note: Some of the sequence  
 CC data for this patent is not represented in the printed specification, but  
 CC is based on sequence information supplied by the European Patent Office.

XX

SQ Sequence 2051 BP; 580 A; 463 C; 474 G; 534 T; 0 U; 0 Other;

Query Match

Best Local Similarity 83.6%; Score 976; DB 9; Length 2051;

Matches 1076; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 91 AGTCTGAAGGGCTCCAGGCTCGCTCAACTGACCGTCTCCAGGGCTGGAAGCTCAT 150

Db |||||

250 AGTCTGAAGGGCTCCAGGCTCGCTCAACTGACCGTCTCCAGGGCTGGAAGCTCAT 309

QY 151 CATGTGGGCTCTCAGTGACATGGTGTCTAAGCGTCAGGCCCATGGAGCCCATCATCAC 210

Db |||||

310 CATGTGGGCTCTCAGTGACATGGTGTCTAAGCGTCAGGCCCATGGAGCCCATCATCAC 369

QY 211 CAATGACCGCTTCACCTCTCAGAGGTACGACAGGGGGGAATTCACCTCGGAGATGAT 270

Db |||||

370 CAATGACCGCTTCACCTCTCAGAGGTACGACAGGGGGGAATTCACCTCGGAGATGAT 429

QY 271 CATCCACAATGTGGAGCCAGTGAATCGGGGAACATCAGATGCGAGCTCCAGAACAGTCG 330

Db |||||

430 CATCCACAATGTGGAGCCAGTGAATCGGGGAACATCAGATGCGAGCTCCAGAACAGTCG 489

QY 331 CTGTCATGGATTCGCTTACCTTACCGTCCAAAGTTATGGGAGAGCTGTTCAATTCACAGTGT 390

Db |||||

490 CTGTCATGGATTCGCTTACCTTACCGTCCAAAGTTATGGGAGAGCTGTTCAATTCACAGTGT 549

QY 391 TAATCTTGTAGTCGTGAGAAATGAACCTTGTGAAGTTACTTGTCTACCCCTCACACTGGAC 450

Db |||||

550 TAATCTTGTAGTCGTGAGAAATGAACCTTGTGAAGTTACTTGTCTACCCCTCACACTGGAC 609

QY 451 CTGGCTCCCGGATATTTCTGGGAGCTCGCTCTCCCTGCTCAGCCATTCAGCTATTTATTT 510

Db |||||

610 CCGGCTCCCGGATATTTCTGGGAGCTCGCTCTCCCTGCTCAGCCATTCAGCTATTTATTT 669

QY 511 TGTTCGGAGCCAGCGACCTTCAAAGTGCAGTGAGCATCTCGCTCTGACCCCAAGAGAG 570

Db |||||

670 TGTTCGGAGCCAGCGACCTTCAAAGTGCAGTGAGCATCTCGCTCTGACCCCAAGAGAG 729

QY 571 CAATGGAGCTTTGACCTTGGTGGCTACCTGGAAGAGCCTGAAAGCCCGCAAGTCTGCAAC 630

Db |||||

730 CAATGGAGCTTTGACCTTGGTGGCTACCTGGAAGAGCCTGAAAGCCCGCAAGTCTGCAAC 789

QY 631 TGTAAATCTCACTGTGATTCGGTGTCCCAAGACACTGGAGGTGTATTAATTTCCAGG 690

Db |||||

790 TGTAAATCTCACTGTGATTCGGTGTCCCAAGACACTGGAGGTGTATTAATTTCCAGG 849

QY 691 TGTATTAACAAGTTTACCAGTTTAGGTTTTCATTTGCTTCTGCGGCAAAAGTCTGGACT 750

Db |||||

850 TGTATTAACAAGTTTACCAGTTTAGGTTTTCATTTGCTTCTGCGGCAAAAGTCTGGACT 909

QY 751 TGGACTAGCAGCAGCATGCTTCTGACGCCGAGTGTACTTTACAATACGCTGCTGCTG 810

Db |||||

910 TGGACTAGCAGCAGCATGCTTCTGACGCCGAGTGTACTTTACAATACGCTGCTGCTG 969

QY 811 CTGCGCGCTGCTGTTGTGGCTGCAACTGCTGCTGCGGTTGTTGTTCTGCTGTAGAG 870

Db |||||

970 CTGCGCGCTGCTGTTGTGGCTGCAACTGCTGCTGCGGTTGTTGTTCTGCTGTAGAG 1029

QY 871 AAAAAAGAGATTCGTATTTCATTTCAAAAGAAATCTGAAAAGAGAGACAAAAGAGA 930

Db |||||

1030 AAAAAAGAGATTCGTATTTCATTTCAAAAGAAATCTGAAAAGAGAGACAAAAGAGA 1089





13-OCT-2003 (first entry)  
Human adult heart cDNA #444.  
Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
genome mapping; biodiversity; genetic disorder.  
Homo sapiens.  
US2003073623-A1.  
17-APR-2003.  
30-JUL-2001; 2001US-00918995.  
30-JUL-2001; 2001US-00918995.  
(DRNA/) DRMANAC R T.  
(LABA/) LABAT I.  
(STAC/) STACHE-CRAIN B.  
(DICK/) DICKSON M C.  
(JONE/) JONES L W.  
Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
WPI; 2003-615964/58.  
New polynucleotide sequences obtained from various cDNA libraries, useful  
as hybridization probes, as oligomers for PCR, for chromosome and gene  
mapping, in the recombinant production of protein, or in generating  
antisense DNA or RNA.  
Claim 1; SEQ ID NO 3342; 44pp; English.  
The invention relates to an isolated polynucleotide comprising any one of  
38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
determined by the technique of SBH (sequencing by hybridisation). Also  
included is a purified polypeptide comprising a sequence corresponding to  
a reading frame of the novel polynucleotide. The nucleic acid sequences  
are useful in diagnostics as expressed sequence tags (EST) for  
identifying expressed genes or for physical mapping of the human genome,  
in forensics, in assessing biodiversity, or in identifying mutations  
responsible for genetic disorders and other traits. The nucleotide  
sequences are also useful as hybridisation probes, as oligomers for PCR,  
for chromosome and gene mapping, in the recombinant production of  
protein, or in generating antisense DNA or RNA. The purified polypeptide  
is useful for generating antibodies specific for it. The present sequence  
is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
for this patent did not form part of the printed specification, but was  
obtained in electronic format directly from USPTO at  
seqdata.uspto.gov/sequence.html?docID=20030073623  
Sequence 474 BP; 154 A; 128 C; 96 G; 95 T; 0 U; 1 Other;  
Query Match 18.6%; Score 217; DB 8; Length 474;  
Best Local Similarity 99.6%; Pred. No. 3e-99;  
Matches 267; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 901 GAAATCTGAAAGAGAGACAAACAAAGAACTGAGACAGAAAGTGAATGAAATCTC 960  
DB 63 GAAATCTGAAAGAGAGACAAACAAAGAACTGAGACAGAAAGTGAATGAAATCTC 122  
QY 961 CGGCTACATTCAGATGACAAAGAACACACAGACACCGCTCTCTCCCTCCCAATCTG 1020  
DB 123 CGGCTACATTCAGATGACAAAGAACACACAGACACCGCTCTCTCCCTCCCAATCTG 182  
QY 1021 TGAATCCAGTATCTGACAAAGAAACAGTAGTGTGTGSCCTCTCTCCACAGCGGCTGA 1080  
DB 183 TGAATCCAGTATCTGACAAAGAAACAGTAGTGTGTGSCCTCTCTCCACAGCGGCTGA 242  
QY 1081 TCAAGCTCCACCGGACGAGGATCATCCAGAGGCTTTTAAATCTGGCCAGCTCTGA 1140  
DB 243 TCAAGCTCCACCGGACGAGGATCATCCAGAGGCTTTTAAATCTGGCCAGCTCTGA 302

QY 1141 GAAGTCAGTAATACTACTGTAGTATAG 1168  
DB 303 GAAGTCAGTAATACTACTGTAGTATAG 330  
RESULT 8  
AAI36582  
ID AAI36582 standard; DNA; 401 BP.  
XX AAI36582;  
AC AAI36582;  
XX 17-OCT-2001 (first entry)  
XX Probe #5268 used to measure gene expression in human placenta sample.  
XX Probe; microarray; human; placenta; antenatal diagnosis;  
KW genetic disorder; ss.  
XX Homo sapiens.  
XX WO200157272-A2.  
XX 09-AUG-2001.  
XX 30-JAN-2001; 2001WO-US000663.  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA Penn SG, Hanzel DK, Chen W, Rank DR;  
PI WPI; 2001-488897/53.  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
gene expression in human placenta.  
PS Claim 25; SEQ ID NO 5268; 654pp; English.  
XX The present invention relates to single exon nucleic acid probes (SENPs).  
CC The present sequence is one such probe. The probes are useful for  
CC producing a microarray for predicting, measuring and displaying gene  
CC expression in samples derived from human placenta. The probes are useful  
CC for antenatal diagnosis of human genetic disorders  
XX SQ Sequence 401 BP; 105 A; 98 C; 111 G; 87 T; 0 U; 0 Other;  
Query Match 16.4%; Score 191; DB 4; Length 401;  
Best Local Similarity 100.0%; Pred. No. 3.4e-85;  
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 44 GGTTCGTGGTCTGTTCACTGACCGTCTCCAGGGCTGGAAGCTCATCATGTGGGCTCTC 103  
DB 211 GGTTCGTGGTCTGTTCACTGACCGTCTCCAGGGCTGGAAGCTCATCATGTGGGCTC 270  
QY 104 TCCAGGGCTCGTTCCTCACTGACCGTCTCCAGGGCTGGAAGCTCATCATGTGGGCTCTC 163  
DB 271 TCCAGGGCTCGTTCCTCACTGACCGTCTCCAGGGCTGGAAGCTCATCATGTGGGCTCTC 330  
QY 164 AGTGACATGGTGTCTTAAGGTCTAGGCGCCATGAGGCCCATCATCAATGACCGCTTC 223  
DB 331 AGTGACATGGTGTCTTAAGGTCTAGGCGCCATGAGGCCCATCATCAATGACCGCTTC 390  
QY 224 ACCTCTCAGAG 234  
DB 391 ACCTCTCAGAG 401











0; Gaps 0;

801 GCTGCTGCTGCTGCCGCCGTCG 822

51 GCTGCTGCTGCTGCCGCCGCTCG 72

Search completed: September 14, 2004, 23:41:48

Job time : 502.037 secs

## RESULT 15

AAV35364

XX

AC AAV35364;

DT 28-SEP-1998 (first entry)

Human GDNF alpha-3 receptor cDNA #1.

XX Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;  
KW treatment; neurodegenerative disease; Parkinson's Disease; ALS; SNA;  
KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;  
KW Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;  
KW muscular dystrophy; diagnostic; ss.

OS Homo sapiens.

XX	Key	Location/Qualifiers
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FT CDS
1. .1200
/*tag= a
/product= "GDNF alpha-3"
/note= "partial sequence
neurotrophic factor alph

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PN  
EP846764-A2.XX  
PD  
10-JUN-1998.

XX 20-NOV-1997; 97EP-00309375.

XX 27-NOV-1996: 96GB-00024677.

PR 09-MAY-1997; 97GB-00009463.

XX PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX  
PI Lawrence GMP;XX  
DR WPT: 1998-299980/27.

DR WPI; 1998-299980/  
DR P-PSDB: AAW65116.

XX New factor alpha 3 receptor polypeptide and e.g. DNA and agonists - used  
PT to treat neuro degenerative diseases, muscular diseases and nerve and  
PT muscle trauma and in diagnostic assays.

xx Claim 9: Fig 1: 22pp; English.

XX This sequence encodes a novel glial cell line-derived neurotrophic factor  
CC alpha-3 receptor (GDNF alpha-3). This protein can be used to treat e.g.  
CC neurodegenerative diseases (such as Parkinson's disease, amyotrophic  
CC lateral sclerosis (ALS), spinal muscular atrophy (SMA), Huntington's  
CC disease, Alzheimer's disease, diabetic neuropathy), muscular diseases  
CC (including the muscular dystrophies) and nerve and muscle trauma and in  
CC diagnostic assays for such conditions

XX  
SO Sequence 1200 BP; 236 A; 419 C; 307 G; 238 T; 0 U; 0 Other;

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 23:14:24 ; Search time 91.2755 Seconds  
(without alignments)  
7101.389 Million cell updates/sec

Title: US-09-729-264-3

Perfect score: 1168

Sequence: 1 agtgcattgtggcaggag.....gtaatacaactgtagtag 1168

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1281558

Minimum DB seq length: 16

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	1.9	1203	3	US-09-220-528-65
2	22	1.9	1699	4	US-09-187-906-20
3	22	1.9	3942	3	US-09-162-484-19
4	21	1.8	550	4	US-09-669-751-128
5	21	1.8	1428	4	US-09-489-039A-3243
6	20	1.7	394	4	US-09-621-976-16752
7	20	1.7	794	4	US-09-621-976-16751
8	20	1.7	984	4	US-09-252-991A-12897
9	20	1.7	1857	4	US-09-252-991A-12897
10	20	1.7	1810	3	US-09-593-711A-3
11	20	1.7	1914	1	US-07-601-094-1
12	20	1.7	1914	1	US-08-012-735-1
13	20	1.7	2214	3	US-08-864-038A-1
14	20	1.7	3331	3	US-08-864-038A-2
15	20	1.7	3331	3	US-08-864-038A-4
16	20	1.7	6407	2	US-08-616-844-7
17	20	1.7	6407	2	US-08-599-654-7
18	20	1.7	6407	3	US-08-944-868A-7
19	20	1.7	6407	3	US-08-944-423A-7
20	20	1.7	6407	3	US-08-944-496-7
21	19	1.6	402	4	US-09-621-976-88
22	19	1.6	1425	1	US-08-464-148-1
23	19	1.6	1425	1	US-08-385-500-1
24	19	1.6	1425	1	US-08-846-784-1
25	19	1.6	1477	4	US-09-620-312D-1019
26	19	1.6	1768	4	US-09-833-381-523
27	19	1.6	1899	4	US-09-919-060-15

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c 28 19 1.6 1899 4 US-09-919-060-16 Sequence 16, Appl
29 19 1.6 1899 1 US-08-447-500-5 Sequence 5, Appl
30 19 1.6 1899 1 US-08-454-097-5 Sequence 5, Appl
31 19 1.6 1899 1 US-08-453-866-5 Sequence 5, Appl
32 19 1.6 1899 3 US-08-185-359-5 Sequence 5, Appl
33 19 1.6 1995 4 US-09-620-312D-908 Sequence 908, App
34 19 1.6 2023 4 US-09-491-522-6 Sequence 6, Appl
35 19 1.6 2115 2 US-08-474-379C-60 Sequence 60, Appl
36 19 1.6 2115 3 US-09-146-249A-60 Sequence 60, Appl
37 19 1.6 2115 3 US-08-206-188B-60 Sequence 60, Appl
38 19 1.6 2439 4 US-09-489-039A-4904 Sequence 4904, Ap
39 19 1.6 2450 4 US-09-491-522-2 Sequence 2, Appl
40 19 1.6 2617 4 US-09-786-240-21 Sequence 21, Appl
41 19 1.6 2693 4 US-09-919-060-12 Sequence 12, Appl
42 19 1.6 2693 4 US-09-919-060-14 Sequence 14, Appl
43 19 1.6 3311 4 US-09-367-891A-5 Sequence 5, Appl
44 19 1.6 5092 3 US-09-412-545-1 Sequence 1, Appl
45 19 1.6 5621 4 US-09-566-921-106 Sequence 106, App

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## ALIGNMENTS

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RESULT 1
US-09-220-528-65
; Sequence 65, Application US/09220528A
; Patent No. 6284540
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor
; FILE REFERENCE: 6029-7998
; CURRENT APPLICATION NUMBER: US/09/220,528A
; EARLIER FILING DATE: 1998-12-24
; EARLIER FILING DATE: 1998-12-24
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-528-65

Query Match 1.9% Score 22; DB 3; Length 1203;
Best Local Similarity 100.0%, Pred. No. 0.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 801 GCTGCTGCTGCTGCTGCCCGCTCG 822
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Db 51 GCTGCTGCTGCTGCTGCCCGCTCG 72

RESULT 2
US-09-187-906-20
; Sequence 20, Application US/09187906
; Patent No. 6671135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/187,906
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/07726
FILING DATE: 07-MAY-97
APPLICATION NUMBER: US 60/017,427
FILING DATE: 08-MAY-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,300
FILING DATE: 07-JUN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,859
FILING DATE: 16-JUL-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043,533
FILING DATE: 10-APR-97
ATTORNEY/AGENT INFORMATION:
NAME: Kaplan, Warren A.
REGISTRATION NUMBER: 34,199
REFERENCE/DOCKET NUMBER: A008 PCT CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-679-2400
TELEFAX: 617-679-2838
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1699 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 175..1374
US-09-187-906-20

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Query Match      1.9%;   Score 22;   DB 4;   Length 1699;
Best Local Similarity 100.0%;   Pred.No. 0.21;
Matches 22;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY      801  GCTGCTGCTGCTGCCGGCGTCG 822
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DB       225  GCTGCTGCTGCTGCCGGCGTCG 246

RESULT 3
US-09-162-484-19
; Sequence 19, Application US/09162484
; Patent No. 6248724
; GENERAL INFORMATION:
; APPLICANT: Phillips, M. Ian
; APPLICANT: Mohuczy, Dagmara
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME MRNA AND METHODS OF USE
; FILE REFERENCE: UFLA:087/UFLA087P
; CURRENT APPLICATION NUMBER: US/09/162,484
; CURRENT FILING DATE: 1998-09-25
; EARLIER APPLICATION NUMBER: 60/059,661
; EARLIER FILING DATE: 1997-09-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 3942
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-162-484-19
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Query Match      1.9%; Score 22; DB 3; Length 3942
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches      22; Conservative 0; Mismatches 0; Indels

QY      801 GCTGCTGCTGCTGCCGCGTGC 822
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DB      72 GCTGCTGCTGCTGCCGCGTGC 93

RESULT 4
US-09-669-751-128/c
; Sequence 128, Application US/09669751
; Patent No. 6551575
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Ralph J.
; TITLE OF INVENTION: Methods for Identifying Compounds for
; TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disor
; TITLE OF INVENTION: Balance and the Perception of Gravity
; FILE REFERENCE: P-NI 3864
; CURRENT APPLICATION NUMBER: US/09/669,751
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 60/168,579
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Drosophila
US-09-669-751-128

Query Match      1.8%; Score 21; DB 4; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches      21; Conservative 0; Mismatches 0; Indels

QY      837 ACTGCTGCTGCCGTGTGTT 857
      |||||||
DB      317 ACTGCTGCTGCCGTGTGTT 297

RESULT 5
US-09-489-039A-3243/c
; Sequence 3243, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES R
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPY
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3243
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3243

Query Match      1.8%; Score 21; DB 4; Length 1428
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches      21; Conservative 0; Mismatches 0; Indels

QY      114 GCTTCAACTGCACCGTCTCCC 134
      |||||||
DB      1147 GCTTCAACTGCACCGTCTCCC 1127

RESULT 6
US-09-621-976-16752
; Sequence 16752, Application US/09621976
; Patent No. 6639063

```

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; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 16752
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-16752

Query Match      1.7%; Score 20; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      810 GCTGCCGCCGTCGTGTGTGT 829
Db      34 GCTGCCGCCGTCGTGTGTGT 53

RESULT 7
US-09-621-976-16751
; Sequence 16751, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 16751
; LENGTH: 794
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-16751

Query Match      1.7%; Score 20; DB 4; Length 794;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      810 GCTGCCGCCGTCGTGTGTGT 829
Db      34 GCTGCCGCCGTCGTGTGTGT 53

US-09-593-711A-3/c
; Sequence 3, Application US/09593711A
; Patent No. 6271030
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
; FILE REFERENCE: RTS-0118
; CURRENT APPLICATION NUMBER: US/09/593,711A
; CURRENT FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 244
; SEQ ID NO 3
; LENGTH: 1910
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
; NAME/KEY: unsure
; LOCATION: 1415
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 1421
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 1422
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 1423

US-09-252-991A-12897
; Sequence 12897, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12735
; LENGTH: 1857
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12735

Query Match      1.7%; Score 20; DB 4; Length 1857;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      827 TGTGGCTGCAACTGCTGCTG 846
Db      1746 TGTGGCTGCAACTGCTGCTG 1765

US-09-593-711A-3/c
; Sequence 3, Application US/09593711A
; Patent No. 6271030
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
; FILE REFERENCE: RTS-0118
; CURRENT APPLICATION NUMBER: US/09/593,711A
; CURRENT FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 244
; SEQ ID NO 3
; LENGTH: 1910
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
; NAME/KEY: unsure
; LOCATION: 1415
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 1421
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 1422
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 1423

US-09-252-991A-12897
; Sequence 12897, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12897
; LENGTH: 984
; TYPE: DNA
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Wed Sep 15 10:41:07 2004

OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 1424  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 1458  
OTHER INFORMATION: unknown  
NAME/KEY: CDS  
LOCATION: (299)...(1336)  
US-09-593-711A-3

Query Match 1.7%; Score 20; DB 3; Length 1910;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 800 CGCTGCTGCTGCTGCCGCG 819  
DB 205 CGCTGCTGCTGCTGCCGCG 185

RESULT 11

US-07-601-094-1/c  
Sequence 1, Application US/07601094  
Patent No. 5215892  
GENERAL INFORMATION:  
APPLICANT: Kishimoto, Tadimitsu  
APPLICANT: Hirano, Toshio  
APPLICANT: Akira, Shizuo  
APPLICANT: Isshiki, Hiroshi  
APPLICANT: Tanabe, Osamu  
APPLICANT: Kinoshita, Shigemi  
APPLICANT: Shinamoto, Takuya  
TITLE OF INVENTION: C/EBP2 Gene and Recombinant  
TITLE OF INVENTION: C/EBP2  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak &  
ADDRESSEE: Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/601,094  
FILING DATE: 19901022  
CLASSIFICATION: 435  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1914 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 281..1316  
OTHER INFORMATION:

Query Match 1.7%; Score 20; DB 1; Length 1914;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 800 CGCTGCTGCTGCTGCCGCG 819  
DB 205 CGCTGCTGCTGCTGCCGCG 185

US-07-601-094-1  
Sequence 1, Application US/07601094  
Patent No. 5215892  
GENERAL INFORMATION:  
APPLICANT: Kishimoto, Tadimitsu  
APPLICANT: Hirano, Toshio  
APPLICANT: Akira, Shizuo  
APPLICANT: Isshiki, Hiroshi  
APPLICANT: Tanabe, Osamu  
APPLICANT: Kinoshita, Shigemi  
APPLICANT: Shinamoto, Takuya  
TITLE OF INVENTION: C/EBP2 Gene and Recombinant  
TITLE OF INVENTION: C/EBP2  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak &  
ADDRESSEE: Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/601,094  
FILING DATE: 19901022  
CLASSIFICATION: 435  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1914 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 281..1316  
OTHER INFORMATION:

Query Match 1.7%; Score 20; DB 1; Length 1914;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 800 CGCTGCTGCTGCTGCCGCG 819  
DB 205 CGCTGCTGCTGCTGCCGCG 185

US-07-601-094-1  
Sequence 1, Application US/07601094  
Patent No. 5215892  
GENERAL INFORMATION:  
APPLICANT: Kishimoto, Tadimitsu  
APPLICANT: Hirano, Toshio  
APPLICANT: Akira, Shizuo  
APPLICANT: Isshiki, Hiroshi  
APPLICANT: Tanabe, Osamu  
APPLICANT: Kinoshita, Shigemi  
APPLICANT: Shinamoto, Takuya  
TITLE OF INVENTION: C/EBP2 Gene and Recombinant  
TITLE OF INVENTION: C/EBP2  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak &  
ADDRESSEE: Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/601,094  
FILING DATE: 19901022  
CLASSIFICATION: 435  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1914 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 281..1316  
OTHER INFORMATION:

QY 800 CGCTGCTGCTGCTGCCGCG 819  
DB 204 CGCTGCTGCTGCTGCCGCG 185

RESULT 12

US-08-012-735-1/c  
Sequence 1, Application US/08012735  
Patent No. 5360894  
GENERAL INFORMATION:  
APPLICANT: Kishimoto, Tadimitsu  
APPLICANT: Hirano, Toshio  
APPLICANT: Akira, Shizuo  
APPLICANT: Isshiki, Hiroshi  
APPLICANT: Tanabe, Osamu  
APPLICANT: Kinoshita, Shigemi  
APPLICANT: Shinamoto, Takuya  
TITLE OF INVENTION: C/EBP2 Gene and Recombinant  
TITLE OF INVENTION: C/EBP2  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak &  
ADDRESSEE: Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/012,735  
FILING DATE: 19930203  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/601,094  
FILING DATE: 22 OCT 1990  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1914 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 281..1316  
OTHER INFORMATION:

Query Match 1.7%; Score 20; DB 1; Length 1914;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 800 CGCTGCTGCTGCTGCCGCG 819  
DB 204 CGCTGCTGCTGCTGCCGCG 185

US-08-012-735-1  
Sequence 1, Application US/08864038A  
Patent No. 6001592  
GENERAL INFORMATION:  
APPLICANT: Kunio NAKASHIMA et al.  
TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

Query Match 1.7%; Score 20; DB 1; Length 1914;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 800 CGCTGCTGCTGCTGCCGCG 819  
DB 204 CGCTGCTGCTGCTGCCGCG 185

RESULT 13

US-08-864-038A-1  
Sequence 1, Application US/08864038A  
Patent No. 6001592  
GENERAL INFORMATION:  
APPLICANT: Kunio NAKASHIMA et al.  
TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

```

; TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
; TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
; TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
; TITLE OF INVENTION: TO SAID POLYPEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: 812-5 Hirano
; STREET: Isshinden
; CITY: Tsu-city
; STATE: Mie-prefecture
; COUNTRY: JAPAN
; ZIP: 514-01
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Word Perfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,038A
; FILING DATE: May 28, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-184459
; FILING DATE: 15-July-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: C. Bruce Hamburg
; REGISTRATION NUMBER: 22,389
; REFERENCE/DOCKET NUMBER: F-5610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)986-2340
; TELEFAX: (212)953-7733
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3331
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Pinctada fucata
; CELL TYPE: mantle epithelial cell
; FEATURE: mRNA
; LOCATION: from 1 to 3331
; IDENTIFICATION METHOD: E (by experiment)
; US-08-864-038A-2

Query Match 1.7%; Score 20; DB 3; Length 3331;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 800 CGTGTGCTGCTGCCGCCG 819
Db 904 CGTGTGCTGCTGCCGCCG 923

RESULT 15
US-08-864-038A-4
; Sequence 4, Application US/08864038A
; Patent No. 6001592
; GENERAL INFORMATION:
; APPLICANT: Kunio NAKASHIMA et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
; TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
; TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
; TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: 812-5 Hirano
; STREET: Isshinden
; CITY: Tsu-city
; STATE: Mie-prefecture
; COUNTRY: JAPAN
; ZIP: 514-01
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Word Perfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,038A
; FILING DATE: May 28, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-184459
; FILING DATE: 15-July-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: C. Bruce Hamburg
; REGISTRATION NUMBER: 22,389
; REFERENCE/DOCKET NUMBER: F-5610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)986-2340
; TELEFAX: (212)953-7733
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2214
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Pinctada fucata
; CELL TYPE: mantle epithelial cell
; US-08-864-038A-1

Query Match 1.7%; Score 20; DB 3; Length 2214;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 800 CGTGTGCTGCTGCCGCCG 819
Db 855 CGTGTGCTGCTGCCGCCG 874

RESULT 14
US-08-864-038A-2
; Sequence 2, Application US/08864038A
; Patent No. 6001592
; GENERAL INFORMATION:
; APPLICANT: Kunio NAKASHIMA et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
; TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
; TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
; TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: 812-5 Hirano
; STREET: Isshinden
; CITY: Tsu-city
; STATE: Mie-prefecture
; COUNTRY: JAPAN
; ZIP: 514-01
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Microsoft Windows 95
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; SOFTWARE: Word Perfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,038A
; FILING DATE: May 28, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-184459
; FILING DATE: 15-July-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: C. Bruce Hamburg
; REGISTRATION NUMBER: 22,389
; REFERENCE/DOCKET NUMBER: F-5610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)986-2340
; TELEFAX: (212)953-7733
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3331
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Pinctada fucata
; CELL TYPE: mantle epithelial cell
; FEATURE: mRNA
; LOCATION: from 1 to 3331
; IDENTIFICATION METHOD: E (by experiment)
; US-08-864-038A-2

Query Match 1.7%; Score 20; DB 3; Length 3331;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 800 CGTGTGCTGCTGCCGCCG 819
Db 904 CGTGTGCTGCTGCCGCCG 923

RESULT 15
US-08-864-038A-4
; Sequence 4, Application US/08864038A
; Patent No. 6001592
; GENERAL INFORMATION:
; APPLICANT: Kunio NAKASHIMA et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
; TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
; TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
; TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: 812-5 Hirano
; STREET: Isshinden
; CITY: Tsu-city
; STATE: Mie-prefecture
; COUNTRY: JAPAN
; ZIP: 514-01
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Word Perfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,038A
; FILING DATE: May 28, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-184459
; FILING DATE: 15-July-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: C. Bruce Hamburg
; REGISTRATION NUMBER: 22,389
; REFERENCE/DOCKET NUMBER: F-5610
; TELECOMMUNICATION INFORMATION:
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 23:16:34 ; Search time 620.673 Seconds  
(without alignments)  
9468.459 Million cell updates/sec

Title: US-09-729-264-3

Perfect score: 1168

Sequence: 1 agtgatcatgggtggcaggag.....gtaatacaactgtatag 1168

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3304383 seqs, 2515761380 residues

Word size : 0

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Minimum DB seq length: 16

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US05\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
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- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
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- 13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10C\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	217	18.6	474	10	US-09-918-995-3342
3	191	16.4	401	9	US-09-864-761-16305
4	25	2.1	357	9	US-09-864-761-16653
5	23	2.0	1284	17	US-10-437-963-81852
6	22	1.9	767	9	US-09-770-445-930
7	22	1.9	1203	9	US-09-220-920-65
8	22	1.9	1829	9	US-09-828-366-15
9	22	1.9	4142	12	US-10-152-319A-1498
10	21	1.8	462	17	US-10-437-963-41506
11	21	1.8	493	10	US-09-918-995-11051
12	21	1.8	550	15	US-10-255-536-128
13	21	1.8	602	17	US-10-767-701-28842
14	21	1.8	1558	10	US-09-930-213-20

C 15	21	1.8	3362	13	US-10-087-192-185	Sequence 185, App
C 16	21	1.8	94917	13	US-10-087-192-184	Sequence 184, App
C 17	20	1.7	330	17	US-10-437-963-55684	Sequence 55684, A
C 18	20	1.7	358	13	US-09-823-245A-58	Sequence 58, Appl
C 19	20	1.7	398	9	US-09-983-965-4945	Sequence 4945, Ap
C 20	20	1.7	412	10	US-09-918-995-5855	Sequence 5855, Ap
C 21	20	1.7	507	17	US-10-430-201-970	Sequence 970, App
C 22	20	1.7	507	17	US-10-430-201-971	Sequence 971, App
C 23	20	1.7	596	17	US-10-767-701-5378	Sequence 5378, Ap
C 24	20	1.7	848	13	US-10-425-114-20418	Sequence 20418, A
C 25	20	1.7	863	13	US-10-027-632-150405	Sequence 150405, A
C 26	20	1.7	863	16	US-10-027-632-150405	Sequence 150405, A
C 27	20	1.7	1192	13	US-10-120-988-90	Sequence 90, Appl
C 28	20	1.7	1255	13	US-10-425-114-19266	Sequence 19266, A
C 29	20	1.7	1290	15	US-10-146-733-16	Sequence 16, Appl
C 30	20	1.7	1383	17	US-10-437-963-37464	Sequence 37464, A
C 31	20	1.7	1526	13	US-10-425-114-31002	Sequence 31002, A
C 32	20	1.7	1576	13	US-09-852-386-87	Sequence 87, Appl
C 33	20	1.7	1737	15	US-10-156-761-3579	Sequence 3579, Ap
C 34	20	1.7	1814	15	US-10-060-036-182	Sequence 182, App
C 35	20	1.7	1910	9	US-09-789-836-1	Sequence 1, Appl
C 36	20	1.7	1910	10	US-09-789-831-1	Sequence 1, Appl
C 37	20	1.7	1910	17	US-10-415-325-18	Sequence 18, Appl
C 38	20	1.7	1943	15	US-10-146-733-14	Sequence 14, Appl
C 39	20	1.7	2080	13	US-10-257-022-30	Sequence 30, Appl
C 40	20	1.7	2504	14	US-10-108-605-246	Sequence 246, App
C 41	20	1.7	2616	17	US-10-437-963-75800	Sequence 75800, A
C 42	20	1.7	2874	9	US-09-801-260-3	Sequence 3, Appl
C 43	20	1.7	2874	15	US-10-145-586-42	Sequence 42, Appl
C 44	20	1.7	3112	16	US-10-120-988-261	Sequence 261, App
C 45	20	1.7	3226	9	US-09-801-260-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-10-104-047-1104  
; Sequence 1104, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20030236392A1el full length cdna  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1104  
; LENGTH: 2051  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-104-047-1104

Query Match	83.6%	Score	976;	DB	16;	Length	2051;
Best Local Similarity	99.8%	Pred. No.	0;				
Matches	1076;	Conservative	0;	Mismatches	2;	Indels	0;
Gaps	0;						
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Db	250	AGTCCTGAAGGGCTCCAGGCTCGCTTCACTGACCGCTCCAGGGCTGGAGCTCAT	309				
QY	151	CATGTGGGCTCTCAGTGACATGGTGTGTAAAGCGTCAGGCCCATGAGCCCATCATCAC	210				
Db	310	CATGTGGGCTCTCAGTGACATGGTGTGTAAAGCGTCAGGCCCATGAGCCCATCATCAC	369				
QY	211	CAATGACCGCTTCACTCTTCAAGGTACGACGAGGGCGGAACTTCACTCGGAGATGAT	270				
Db	370	CAATGACCGCTTCACTCTTCAAGGTACGACGAGGGCGGAACTTCACTCGGAGATGAT	429				
QY	271	CATCCAAATGTGGAGCCCATGATTTCGGGGACATCAGATGACGCTCCAGCAACAGTCG	330				



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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16653
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF064857.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.93
US-09-864-761-16653

Query Match          2.1%; Score 25; DB 9; Length 357;
Best Local Similarity 100.0%; Pred.No. 0.043;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      877 AGGATTTTCGTATTCAATTTCAAAG 901
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Db       42 AGGATTTTCGTATTCAATTTCAAAG 66

RESULT 5
US-10-437-963-81852/c
; Sequence 81852, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 81852
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_81337C.1
US-10-437-963-81852

Query Match          2.0%; Score 23; DB 17; Length 1284;
Best Local Similarity 100.0%; Pred.No. 0.48;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 800 CGCTGCTGCTGCTGCCGCGCTGC 822  
Db 156 CGCTGCTGCTGCTGCCGCGCTGC 134

## RESULT 6

US-09-770-445-930  
; Sequence 930, Application US/09770445  
; Patent No. US20020023281A1  
; GENERAL INFORMATION:  
; APPLICANT: Gorlach, Jorn  
; APPLICANT: An, Yong-Qiang  
; APPLICANT: Hamilton, Carol M.  
; APPLICANT: Price, Jennifer L.  
; APPLICANT: Raines, Tracy M.  
; APPLICANT: Yu, Yang  
; APPLICANT: Rameaka, Joshua G.  
; APPLICANT: Page, Amy  
; APPLICANT: Matthew, Abraham V.  
; APPLICANT: Ledford, Brooke L.  
; APPLICANT: Woessner, Jeffrey P.  
; APPLICANT: Haas, William David  
; APPLICANT: Garcia, Carlos A.  
; APPLICANT: Krickler, Maja  
; APPLICANT: Slader, Ted  
; APPLICANT: Davis, Keith R.  
; APPLICANT: Allen, Keith  
; APPLICANT: Hoffman, Neil  
; APPLICANT: Hurban, Patrick  
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
; FILE REFERENCE: thaliana  
; CURRENT APPLICATION NUMBER: US/09/770,445  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/178,472  
; PRIOR FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 999  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 930  
; LENGTH: 767  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-770-445-930

Query Match 1.9%; Score 22; DB 9; Length 767;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 814 CGCGCGCTGTTGTTGGCTGC 835  
Db 672 CGCGCGCTGTTGTTGGCTGC 693

## RESULT 7

US-09-220-920-65  
; Sequence 65, Application US/09220920  
; Patent No. US2002002269A1  
; GENERAL INFORMATION:  
; APPLICANT: Milbrandt, Jeffrey D.  
; APPLICANT: Baloh, Robert H.  
; TITLE OF INVENTION: Artemin, A No. US2002002269A1 Neurotrophic Factor  
; FILE REFERENCE: 6029-7996  
; CURRENT APPLICATION NUMBER: US/09/220,920  
; CURRENT FILING DATE: 1998-12-24  
; EARLIER APPLICATION NUMBER: 09/163,283  
; EARLIER FILING DATE: 1998-09-29  
; EARLIER APPLICATION NUMBER: 60/108,148  
; EARLIER FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: 09/218,698  
; EARLIER FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 65  
; LENGTH: 1203  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-220-920-65

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Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 801 GCTGCTGCTGCTGCCGCGCTGC 822  
Db 51 GCTGCTGCTGCTGCCGCGCTGC 72

## RESULT 8

US-09-828-366-15  
; Sequence 15, Application US/09828366  
; Patent No. US20020010137A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Klein, Robert D.  
; APPLICANT: Napier, Mary  
; APPLICANT: Wood, William I.  
; APPLICANT: Yuan, Jean  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC  
; FILE REFERENCE: P1694R1C1  
; CURRENT APPLICATION NUMBER: US/09/828,366  
; CURRENT FILING DATE: 2001-04-05  
; Prior filing data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 29  
; SEQ ID NO 15  
; LENGTH: 1829  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-828-366-15

Query Match 1.9%; Score 22; DB 9; Length 1829;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 801 GCTGCTGCTGCTGCCGCGCTGC 822  
Db 88 GCTGCTGCTGCTGCCGCGCTGC 109

## RESULT 9

US-10-152-319A-1498  
; Sequence 1498, Application US/10152319A  
; Publication No. US20040072160A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Porter, Mark  
; APPLICANT: Johnson, Kory  
; APPLICANT: Higgs, Brandon  
; APPLICANT: Castie, Arthur  
; APPLICANT: Elashoff, Michael  
; TITLE OF INVENTION: Molecular Toxicology Modeling  
; FILE REFERENCE: 44921-5089-US  
; CURRENT APPLICATION NUMBER: US/10/152,319A  
; CURRENT FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: US 60/292,335  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/297,523  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,925  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 60/303,810  
; PRIOR FILING DATE: 2001-07-10

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; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/330,462
; PRIOR FILING DATE: 2001-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1498
; LENGTH: 4142
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_012544
US-10-152-319A-1498

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Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      801 GCTGCTGCTGCTGCCGCGTCG 822
Db      95 GCTGCTGCTGCTGCCGCGTCG 116

RESULT 10
US-10-437-963-41506/c
; Sequence 41506, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 41506
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_44844C.1
US-10-437-963-41506

Query Match      1.8%; Score 21; DB 17; Length 462;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      802 CTGCTGCTGCTGCCGCGTCG 822
Db      133 CTGCTGCTGCTGCCGCGTCG 113

RESULT 11
US-09-918-995-11051/c
; Sequence 11051, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
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; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11051
; LENGTH: 493
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(493)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-11051

Query Match      1.8%; Score 21; DB 10; Length 493;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      804 GCTGCTGCTGCCGCGTCGTT 824
Db      443 GCTGCTGCTGCCGCGTCGTT 423

RESULT 12
US-10-255-536-128/c
; Sequence 128, Application US/10255536
; Publication No. US20030087807A1
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Ralph J.
; TITLE OF INVENTION: Methods for Identifying Compounds for
; TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to
; TITLE OF INVENTION: Balance and the Perception of Gravity
; FILE REFERENCE: P-NI 3864
; CURRENT APPLICATION NUMBER: US/10/255,536
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US/09/669,751
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 60/168,579
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Drosophila
US-10-255-536-128

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Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      837 ACTGCTGCTGCCGTTGTTGTT 857
Db      317 ACTGCTGCTGCCGTTGTTGTT 297

RESULT 13
US-10-767-701-28842/c
; Sequence 28842, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
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; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 28842  
; LENGTH: 602  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 8088472  
US-10-767-701-28842

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 803 TGTGCTGCTGCCGCGTGT 823  
DB 206 TGTGCTGCTGCCGCGTGT 186

## RESULT 14

US-09-930-213-20/c  
; Sequence 20, Application US/09930213  
; Publication No. US20030170625A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSENTHAL, ANDRE  
; APPLICANT: HINZMANN, BERND  
; APPLICANT: SCHAFER, REINHARD  
; APPLICANT: ZUBER, JOHANNES  
; APPLICANT: TICHE-NITSE, OLEG  
; APPLICANT: GRIPS, MARTIN  
; APPLICANT: HELLMER, MARTIN  
; APPLICANT: SCHMITZ, ANNE-CHANTAL  
; APPLICANT: SERS, CHRISTINE  
; TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS  
; FILE REFERENCE: ALBRE-14  
; CURRENT APPLICATION NUMBER: US/09/930,213  
; CURRENT FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: DE 10004102.7  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 885  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 1558  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
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; OTHER INFORMATION: a, t, c, g, other or unknown  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (427)  
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; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (492)  
; OTHER INFORMATION: a, t, c, g, other or unknown  
; FEATURE:  
; NAME/KEY: modified\_base  
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; OTHER INFORMATION: a, t, c, g, other or unknown  
US-09-930-213-20

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Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 801 GCTGCTGCTGCTGCCGCGTC 821  
DB 223 GCTGCTGCTGCTGCCGCGTC 203

## RESULT 15

US-10-087-192-185/c  
; Sequence 185, Application US/10087192  
; Publication No. US20020182586A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
; TITLE OF INVENTION: CANCER  
; FILE REFERENCE: 529452000122  
; CURRENT APPLICATION NUMBER: US/10/087,192  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 2059  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 185  
; LENGTH: 3362  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-087-192-185

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Best Local Similarity 100.0%; Pred. No. 5.3;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 947 GCTGCTGCTGCTGCCGCGTC 927

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Job time : 620.673 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Perfect score: 1240

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Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

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Minimum DB seq length: 16

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33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

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36: em\_htg\_mam.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1125	90.7	2051	6	AX747579	Sequence
3	1125	90.7	2051	6	AK092516	Homo sapi
4	1074	86.6	1175	6	AX380396	Sequence
5	976	78.7	1168	6	AX380398	Sequence
6	739	59.6	1139	6	AX380402	Sequence
7	302	24.4	142742	9	AF121782	Sequence
8	302	24.4	340000	9	HS21C080	Homo sapi
9	200	16.1	182532	9	CH179K04	Homo sapi
10	145	11.7	156288	9	BS000162	Pan trogl
11	119	9.6	40205	9	AF045450	Homo sapi
12	119	9.6	170121	9	AF064860	Homo sapi
13	100	8.1	199665	9	AF064857	Homo sapi
14	72	5.8	192219	9	RP43002119	Homo sapi
15	25	2.0	6470	3	AB090820	Anopheles
16	24	1.9	5178	3	AY119603	Drosophila
17	24	1.9	8152	3	DMTOC	Human DNA
18	24	1.9	55256	9	HSJ735G18	Human DNA
19	24	1.9	59693	2	AC099814	Homo sapi
20	24	1.9	77137	3	AC004422	Drosophila
21	24	1.9	83876	2	AC020009	Drosophila
22	24	1.9	94296	2	AL160261	Homo sapi
23	24	1.9	111645	9	AL138767	Human DNA
24	24	1.9	136746	2	AC006191	Homo sapi
25	24	1.9	148102	8	AP003328	Oryza sat
26	24	1.9	148762	8	AP002843	Oryza sat
27	24	1.9	161529	9	AP001998	Homo sapi
28	24	1.9	169931	3	AC008321	Drosophila
29	24	1.9	171400	9	AP006437	Homo sapi
30	24	1.9	181585	9	AL139350	Human DNA
31	24	1.9	184554	3	AC099022	Drosophila
32	24	1.9	196857	9	AC027239	Homo sapi
33	24	1.9	206773	2	AC010932	Homo sapi
34	24	1.9	268984	3	AE001274	Leishmani
35	24	1.9	314957	3	AE003581	Drosophila
36	24	1.9	342614	2	AC108705	Homo sapi
37	23	1.9	1155	10	AFS37215	Mus muscu
38	23	1.9	1195	6	AX380404	Sequence
39	23	1.9	29865	2	AC020047	Drosophila
40	23	1.9	100494	9	HSJ514B11	Human DNA
41	23	1.9	106256	3	AC108135	Leishmani
42	23	1.9	124612	2	AC105442	Leishmani
43	23	1.9	138764	9	AC006387	Homo sapi
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

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Sequence 5 from Patent WO0200710.  
AX380400  
AX380400.1 GI:19575330  
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Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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Welcher,A.A., Sarmiento,U.M., Schultz,H.J. and Chute,H.T.  
B7-like molecules and uses thereof  
Patent: WO 0200710-A 5 03-JAN-2002;

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Sequence 5 from Patent WO0200710.  
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AX380400.1 GI:19575330  
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Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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Welcher,A.A., Sarmiento,U.M., Schultz,H.J. and Chute,H.T.  
B7-like molecules and uses thereof  
Patent: WO 0200710-A 5 03-JAN-2002;

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		/note="unnamed protein product"	
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Qy	61	AACCTGGTGGCTTAGAACAAATGAAAGGCCATTTGCTACGGTTCAGAGCTGTAGTTTC	120
Db	61	AACCTGGTGGCTTAGAACAAATGAAAGGCCATTTGCTACGGTTCAGAGCTGTAGTTTC	120
Qy	121	TGGGTCTGTGTAAGTCAATAGAGCCGCCAGAAATGCAACAGTCTGAGAGGCTCCCA	180
Db	121	TGGGTCTGTGTAAGTCAATAGAGCCGCCAGAAATGCAACAGTCTGAGAGGCTCCCA	180
Qy	181	GGCTCGCTTCAACTGCACCGCTCTCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGA	240
Db	181	GGCTCGCTTCAACTGCACCGCTCTCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGA	240
Qy	241	CATGTGTGCTAAGCGTCAAGCCCATGGAGCCCATCATCAACAAATGACCGTTCAGCTC	300
Db	241	CATGTGTGCTAAGCGTCAAGCCCATGGAGCCCATCATCAACAAATGACCGTTCAGCTC	300
Qy	301	TCAGAGTACGACAGCGCGGGAACCTTCACTCGAGATGATCATCACAAATGTGGAGCC	360
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Qy	361	CAGTGTATCGGGGAACATCAGATGCAGCTCCAGAACAGTCGCGCTGCATGGATCTGCTTA	420
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Qy	481	GAATGAACTTGTGAAGTACTTGTCTACCTCATCATCGGACCGGCTCCGGATATTTC	540
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Qy	541	CTGGAGCTCGGTCTCTCGTTCAGCCATTAAGCTATTATTTTGTTCGGAGCCCGAGCGA	600
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Db	601	CTTTCAAAGTGCAGTGAAGCTCTCGGCTCTGACCCACAGAGCAATGGAGCTTGACTTG	660
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LOCUS		Sequence 1104 from Patent EPI308459.	PAT 20-JUN-2003
DEFINITION		AX747579	
ACCESSION		AX747579	
VERSION		AX747579.1	GI:32131967
KEYWORDS		Homo sapiens (human)	
SOURCE		Homo sapiens	
ORGANISM		Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1	
AUTHORS		Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and Masuko, Y.	
TITLE		Full-length cDNA sequences	
JOURNAL		Patent: EP 1308459-A 1104 07-MAY-2003;	
		Helix Research Institute (JP) ; Research Association for	
		Biotechnology (JP)	
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Best Local Similarity		100.0%; Pred. No. 0;	
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Db	203	GGTTCCTGGGTCTGGTAATGAAGTCATAGAAGGCCCGCCAGATGCAACAGTCTCTGAAGGCG	262
Qy	176	TCCAGGCTCGCTTCAACTGACCGTCTCCAGGGCTGGAAGCTCATCATGTGGGCTCTC	235

Db 263 TCCAGAGCTCGGTTCAACTGCAACCTCTCCAGGCTGGAAGCTCATCATGTGGGCTCTC 322  
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 QY 296 ACCTCTCAGAGTACGACAGGCGGGAACCTTCACTCGGAGATGATCATCCACAAATGTG 355  
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 QY 416 GCTTACCTTACCGTCCAAAGTTATGGAGAGCTGTTTCACTCCAGTGTAACTTGTAGTC 475  
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 QY 476 GCTGAGATGAACCTTGTGAAGTTACTTGTCTACCCCTCACACTGGACCGGCTCCCGAT 535  
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RESULT 3

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 LOCUS Homo sapiens cDNA FLJ35197 fis, clone PLACB6017788, highly similar to IGSP5.  
 DEFINITION AK092516  
 ACCESSION AK092516  
 VERSION GI:21751130  
 KEYWORDS oligo capping; fis (full insert sequence).  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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 Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R., Otaki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.  
 NEDO human cDNA sequencing project  
 Unpublished  
 2 (bases 1 to 2051)  
 Isogai, T. and Yamamoto, J.  
 Direct Submission  
 Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan  
 (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
 NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB;  
 annotation: HRI and RAB.  
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 QY 236 AGTGACATGGTGGTGTCTAAGCGCTCAGGCGCCATGAGCCCATCATCAACATGACCGCTTC 295  
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 QY 296 ACCTCTCAGAGTACGACAGGCGGGAACCTTCACTCGGAGATGATCATCCACAAATGTG 355  
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[illegible]

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Qy	1076	CTCCCTCCCAATCTCTGTGAATCCAGTGATCCTGAAACAAAGAAACAGTAGCTGTGGCCCT	1135
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Qy	1136	CCTCACCAGCGGCTGATCAACGTCACCCAGGCGCAGCAAGTCATCCACAGGCTTCTTTT	1195
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Qy	1196	AATCTGGCCAGTCTCTGAGAGGTCAGTAATACAACTGTAGTATAG	1240
Db	1131	AATCTGGCCAGTCTCTGAGAGGTCAGTAATACAACTGTAGTATAG	1175
RESULT 5			
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LOCUS	AX380398	1168 bp	DNA linear PAT 18-MAR-2002
DEFINITION	Sequence 3 from Patent WO0200710.		
ACCESSION	AX380398		
VERSION	AX380398.1 GI:19575328		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1		
TITLE	Welcher,A.A., Sarmiento,U.M., Schultz,H.J. and Chute,H.T.		
JOURNAL	B7-like molecules and uses thereof		
	Patent: WO 0200710-A 3 03-JAN-2002;		
	Angen, Inc. (US)		
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Qy	223	CATGTGGGCTCTCAGTGACATGTGGTCTTAAGGCTCAGGCCCATGAGGCCCATCATCAC	282
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Qy	343	CATCCAAATGTGGAGCCAGTGAATCGGGGAAACATCAGATGACGCTCCAGAAACAGTCG	402
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Qy	403	CTGTCATGGATCTGCTTACCTTACCGTCCAAAGTTATGGGAGAGCTGTTCAATCCAGTGT	462
Db	331	CTGTCATGGATCTGCTTACCTTACCGTCCAAAGTTATGGGAGAGCTGTTCAATCCAGTGT	390
Qy	463	TAATCTTGTAGTCTGCTGAGAAATGAACCTTGTGAAGTTACTTGTCTACCTCACACTGAC	522
Db	391	TAATCTTGTAGTCTGCTGAGAAATGAACCTTGTGAAGTTACTTGTCTACCTCACACTGAC	450
Qy	523	CCGGCTCCCGGATATTTCTTGGGAGCTCGGTCTCTCTGGTCAAGCAATCAAGCTATTATTT	582
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Qy	583	TGTTCCGGAGCCCGAGCAACCTTCAAGTGCAGTGAGCATCTCTGCTCTGACCCACAGAG	642
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Qy	703	TGTAATCTCACTGTGATTCGGTGTCCCAAGACACTGGAGGTGGTATTATATTCAGG	762
Db	631	TGTAATCTCACTGTGATTCGGTGTCCCAAGACACTGGAGGTGGTATTATATTCAGG	690
Qy	763	TGTAATCTCAAGTTTACCGAGTTTAGTCTTCTTCAATGCTTCTGGGGCAAGTTGGAAT	822
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Qy	883	CTCCGCGCTGCTTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	942
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LOCUS	AX380402	1139 bp	DNA linear PAT 18-MAR-2002
DEFINITION	Sequence 7 from Patent WO0200710.		
ACCESSION	AX380402		
VERSION	AX380402.1 GI:19575332		
KEYWORDS	Homo sapiens (human)		
SOURCE			

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Welcher, A.A., Sarmiento, U.M., Schultz, H.J. and Chute, H.T.  
TITLE B7-like molecules and uses thereof  
JOURNAL Patent: WO 020710-A 7 03-JAN-2002;  
Amgen, Inc. (US)  
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Query Match 59.6%; Score 739; DB 6; Length 1139;  
Best Local Similarity 99.9%; Pred. No. 0;  
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DB 84 AGTCCTGAAGGCTCCAGGCTCGCTCACTCAGCGCTCCAGGCTGGAAGTCTCAT 143  
QY 223 CATGTGGGCTCTCAGTGACATGTGTGCTTAAGCGTCAGGCCCATGAGCCCATCATCAC 282  
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QY 283 CAATGACCGCTTCACTCTCAGAGGTACGACCGAGGGGGGAACCTTCACTCGGAGATGAT 342  
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LOCUS Homo sapiens chromosome 21q22.3 PAC 206A10, complete sequence.  
DEFINITION  
ACCESSION AF121782  
VERSION AF121782.1 GI:4210991  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 142742)  
AUTHORS Taudien, S., Dagand, E., Hildmann, T., Nordsiek, G., Drescher, B.,  
Schattveyor, R., Weber, J., Schilling, M., Menzel, U., Yaspo, M.L. and  
Rosenthal, A.  
TITLE Direct Submission  
JOURNAL Submitted (21-JAN-1999) Genome Analysis, Institute for Molecular  
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany  
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Best Local Similarity 100.0%; Pred. No. 6.4e-168; Indels 0; Gaps 0;
Matches 302; Conservative 0; Mismatches 0;

QY 433 AGTTATGGAGAGCTGTTTCATTTCCAGTGTGTTAATCTGTAGTCGCTGAGAATGAACCTTGG 492
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QY 493 TGAAGTTACTTGTCTACCTCCACACTGGACCCCGCTCCGGATATTTCTCGGAGCTCGG 552
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QY 553 TCTCCTGGTCAGCATTCAAGCTATTTATTTGTTCCGAGCCCGAGCAGCTTCAAAAGTGC 612
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QY 613 AGTGAGCATCTCGGCTCTGACCCCAAGCAATGGACTTTGACTTGGTGCTACCTG 672
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QY 673 GAAGAGCCTGAAGCCCGCAAGTCTGCACTGTAATCTCAGTGTGTTGGTGTCCTCCCA 732
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QY 733 AG 734
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Db 49954 AG 49955

RESULT 8
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LOCUS Homo sapiens chromosome 21 segment HS21C080.
ACCESSION AL163280 AP001735 BA000005
VERSION AL163280.2 GI:7717369
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 340000)
Hattori,M., Fujiyama,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
Park,H.S., Toyoda,A., Sakaki,Y., Taudien,S., Blechschmidt,K.,
Ohki,M., Takagi,T., Sakagi,Y., Kumpf,K., Lehmann,R.,
Polley,A., Menzel,U., Delabar,J., Kumpf,K., Schillhabel,M., Schudy,A.,
Fatterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A.,
Zimmermann,W., Rosenthal,A., Sasaki,T., Nagamine,K., Mitsuoyama,S.,
Aakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuoyama,S.,
Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsieck,G.,
Hornischter,K., Brandt,P., Scharfe,M., Schoen,O., Desario,A.,
Reichelt,J., Kauer,G., Bloeker,H., Ramser,J., Beck,A., Klages,S.,
Hennig,S., Riesselmann,L., Dagand,E., Wehrmeyer,S., Borzym,K.,
Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
Yaspo,M.I.
Direct Submission
Submitted (05-MAY-2000) The Chromosome 21 Mapping and Sequencing
Consortium: * RIKEN Genomic Sciences Center, Human Genome Research
Group * Institute of Molecular Biotechnology, Genome Analysis *
Keio University School of Medicine, Dept. of Molecular Biology *
GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular
Genetics (addresses see below)
The Chromosome 21 Mapping and Sequencing Consortium consists of
* RIKEN Genomic Sciences Center, Human Genome Research Group, *
Sagamihara 228-8555, Japan,
* e.mail: sakaki@gsc.riken.go.jp
* URL: http://hgp.gsc.riken.go.jp/
and
* Institute of Molecular Biotechnology, Genome Analysis, *
Beutenbergstrasse 11, D-07745 Jena, Germany,
* e.mail: gscj-submit@genome.imb-jena.de
* URL: http://genome.imb-jena.de/
and
* Keio University School of Medicine, Dept. of Molecular Biology, *

```

Tokyo 160-8582, Japan,  
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 and  
 \* GBF, Dept. of Genome Analysis,  
 \* Mascheroder Weg 1, D-38124 Braunschweig, Germany, \* e.mail:  
 info.genome@gbf.de  
 \* URL: http://genome.gbf.de/  
 and  
 \* Max-Planck Institute for Molecular Genetics,  
 \* Inneistrasse 73, D-14195 Berlin, Germany,  
 \* e.mail: info.chr21@molgen.mpg.de  
 \* URL: http://chr21.rz-berlin.mpg.de/.

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repeat\_region

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Query Match 24.4% Score 302; DB 9; Length 340000;
Best Local Similarity 100.0%; Pred. No. 6.9e-168; Indels 0; Gaps 0;
Matches 302; Conservative 0; Mismatches 0;

Qy 433 AGTTATGGGAGAGCTGTTCAATCCAGTGTAACTTTGTAGTCGCTGAGAAATGAACCTTG 492
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Qy 553 TCTCCTGCTCAGCCATTCAAGCTATTATTTGTTCCGGAGCCAGCCAGCTTCAAAGTGC 612
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Db 274074 GAAGAGCTGAAGCCCGGCAAGTCTGCAACTGTAATCTCAGTGTGATTCGGTGTCCCCA 274133

Qy 733 AG 734
Db 274134 AG 274135

RESULT 9
CH179K04 182532 bp DNA linear PRI 16-OCT-2003
LOCUS Pan troglodytes chromosome 22 BAC CH251-179K04, complete sequence.
ACCESSION AL954228
VERSION AL954228.1 GI:37619870
KEYWORDS HTG.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE
AUTHORS The Chimpanzee Chromosome 22 Sequencing Consortium
CONSTRM Chimpanzee chromosome 22 genomic sequence
TITLE Unpublished
JOURNAL 2 (bases 1 to 182532)
REFERENCE 2 (bases 1 to 182532)
AUTHORS Schafhe, M., Berg, C., Conrad, A., Hornischer, K., Loehnert, T.H.,
Ludwig, M., Thies, S., Weber, K. and Bloecker, H.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-2003) GSF, Dept. of Genome Analysis, Mascheroder
Weg 1, D-38124 Braunschweig, Germany, E-mail: info.genome@gsf.de
COMMENT The Chimpanzee Chromosome 22 Sequencing Consortium consists of :
Shanghai, China
Taiwan;
----- Genome Center
Center: GSF, Braunschweig
Center code: GSF
Web site: http://genome.gsf.de/
Contact: info.genome@gsf.de
----- Project Information

```



```

Db      1 GAGTCGGTCTCTGGTCAGCCATTCAAGCTATTATTTTGTTCGGAGCCGAGGACCTT 60
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VERSION      AF045450.1 GI:2895783
KEYWORDS      HTG.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 40205)
AUTHORS      Taudien,S. and Rosenthal,A.
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 40205)
AUTHORS      Taudien,S., Nordsiek,G., Dagand,E., Hildmann,T., Drescher,B.,
Weber,J., Rosenthal,A. and Yaspo,M.L.
TITLE      Submitted (29-JAN-1998) Genome Analysis, Institut for Molecular
JOURNAL      Biotechnology, Heutenbergstrasse 11, Jena 07745, Germany
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Qy 61 AACCTGGTGGCTTAGAACAAATGAAAGGCAATTGCTCAGGTTCCAGAAAGCTGTAGGTT 119  
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LOCUS AF064860  
DEFINITION HTG; HTGS DRAFT.  
ACCESSION AF064860.2 GI:18958624  
VERSION AF064860  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 170121)  
AUTHORS Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T., Park,H.-S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.-K., Soeda,E., Onki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K., Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R., Patterson,D., Reichwald,K., Rump,A., Schillhabel,M.B., Schudy,A., Zimmermann,W., Rosenthal,A., Kudoh,J., Kawasaki,K., Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyama,S., Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G., Horisicher,K., Brandt,P., Scharfe,M., Schoen,O., Desario,A., Reichelt,J., Kauer,G., Bloecker,H., Ramser,J., Beck,A., Klages,S., Hennig,S., Riesselmann,L., Dagand,E., Haaf,T., Wehmeyer,S., Borzym,K., Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and Yaspo,M.Laure.  
The DNA sequence of human chromosome 21  
Nature 405 (6784), 311-319 (2000)  
2089799  
10830953  
REFERENCE 2 (bases 1 to 170121)  
AUTHORS Rump,A., Dagand,E., Hildmann,T., Nordsiek,G., Drescher,B., Weber,J., Schattevoy,R., Yaspo,M.-L. and Rosenthal,A.  
Direct Submission  
TITLE Submitted (12-MAY-1998) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany  
JOURNAL 3 (bases 1 to 170121)  
REFERENCE 3 (bases 1 to 170121)  
AUTHORS Rump,A., Dagand,E., Hildmann,T., Nordsiek,G., Drescher,B., Weber,J., Schattevoy,R., Yaspo,M.-L., Rosenthal,A., Yaspo,M.-L. and Rosenthal,A.  
Direct Submission  
TITLE Submitted (27-FEB-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena 07745, Germany  
JOURNAL 4 (bases 1 to 170121)  
REFERENCE 4 (bases 1 to 170121)  
AUTHORS Rump,A., Dagand,E., Hildmann,T., Nordsiek,G., Drescher,B., Weber,J., Schattevoy,R., Yaspo,M.-L. and Rosenthal,A.  
Direct Submission  
TITLE Submitted (05-MAR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena 07745, Germany  
JOURNAL On Feb 27, 2002 this sequence version replaced gi:3171153.  
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Db 159504 AACCTGGTGGCTTAGAACAATGGAAGGCATTTGTCACGGTTCACGAAGCTGTAGGTT 159562
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RESULT 13
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LOCUS Homo sapiens BAC derived from chromosome 21q22.3, complete
DEFINITION sequence, containing PEP19 (PCP4) gene.
ACCESSION AF064857
VERSION AF064857.1 GI:3171149
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 199665)
AUTHORS Taudien,S., Nordsiek,G., Korenberg,J., Drescher,B., Weber,J.,
Schattvey,R. and Rosenthal,A.
TITLE Direct Submission
JOURNAL Submitted (11-MAY-1998) Genome Analysis, Institute for Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
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Db 17555 CCAGCGGCTGATCAAGTCCACCCAGGCCAGCAAGTCATCCACAGGCTCTTTTAAATCT 17614

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QY 1201 GGCCAGTCTCGAAGGTCAGTAATACAACTGTAGTATAG 1240
Db 17615 GGCCAGTCTCGAAGGTCAGTAATACAACTGTAGTATAG 17654

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Pan troglodytes chromosome 22 BAC RP43-002119, complete sequence.
ACCESSION AL954227
VERSION AL954227.3 GI:38453654
KEYWORDS HTG.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 192219)
AUTHORS The Chimpanzee Chromosome 22 Sequencing Consortium.
TITLE The Chimpanzee Chromosome 22 genomic sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 192219)
AUTHORS Scharfe, M., Berg, C., Conrad, A., Hornischer, K., Loehnert, T.H.,
Ludwig, M., Thies, S., Weber, K. and Bloecker, H.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2003) GBF, Dept. of Genome Analysis, Mascheroder
Weg 1, D-38124 Braunschweig, Germany, E-mail: info.genome@gbf.de
COMMENT On Nov 19, 2003 this sequence version replaced gi:38228900.
The Chimpanzee Chromosome 22 Sequencing Consortium consists of :
*Chinese National Human Genome Center at Shanghai,
Shanghai, China
*GBF, Dept. of Genome Analysis, Braunschweig, Germany; *Institute
of Molecular Biotechnology, Jena, Germany; *KRIBB Genome Research
Center, Daejeon, Korea;
*Max-Planck Institute for Molecular Genetics, Berlin, Germany;
*National Institute of Genetics, Mishima, Japan;
*National Yang Ming University Genome Research Center, Taipei,
Taiwan;
*RIKEN Genomic Sciences Center, Yokohama, Japan.
PROGRAMS AND PARAMETERS USED FOR ANNOTATION:
+ Analysis and annotation were performed with the automatic
+ 'first-pass' annotation and submission tool
+ 'AnnoMitter' (Hornischer & Bloecker).
+ Programs used by 'AnnoMitter':
+ ----- Genome Center
Center: GBF, Braunschweig
Center code: GBF
Web site: http://genome.gbf.de/
Contact: info.genome@gbf.de
----- Project Information
Center project name:
Center clone name: RP43-002119
----- Summary Statistics
Sequencing vector: ##;
Chemistry: Dye-terminator-amersham: ## of reads
Chemistry: Dye-primer-amersham: ## of reads
Assembly program: ##
Consensus quality: 0 bases at least Q40
Consensus quality: 0 bases at least Q30
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Estimated insert size: ##; agarose-fp estimation
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Db 191622 GGGAACTTCACCTCGGAGATCATCCACATGTGGAGCCAGTGATTCGGGGAACATC 191681  
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QY 380 AGATGCAGCCTC 391  
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Db 191682 AGATGCAGCCTC 191693  
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RESULT 15  
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LOCUS  
DEFINITION Anopheles gambiae retrotransposon R7Ag1 DNA, linear INV 25-MAR-2003  
ACCESSION AB090820  
VERSION AB090820.1 GI:28569877  
KEYWORDS  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM  
Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;  
Anopheles.

REFERENCE 1  
AUTHORS Kojima, K. and Fujiwara, H.  
TITLE Evolution of Target Specificity in R1 Clade Non-LTR  
Retrotransposons  
JOURNAL Mol. Biol. Evol. 20 (3), 351-361 (2003)  
MEDLINE 22531580  
PUBMED 12644555

REFERENCE 2 (bases 1 to 6470)  
AUTHORS Kojima, K. and Fujiwara, H.  
TITLE Direct Submission  
JOURNAL Submitted (26-AUG-2002) Kenji K Kojima, University of Tokyo,  
Department of Integrated Biosciences, Graduate School of Frontier  
Sciences, Bioscience Building 501, 5-1-5 Kashiwanoha, Kashiwa,  
Chiba 277-8562, Japan (E-mail:kk27513@mail.ecc.u-tokyo.ac.jp,  
Tel:81-4-7136-3661, Fax:81-4-7136-3660)  
Location/Qualifiers

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PS Claim 1; Fig 3; 135pp; English.

XX The invention relates to an isolated B7-like (B7-L) polypeptide (I). The  
CC polypeptide, polynucleotide encoding it and antibody against (I) are  
CC useful for treating B7-like polypeptide-related disease, disorders or  
CC conditions including reproductive disorders (e.g. infertility,  
CC miscarriage, preterm labour and delivery and endometriosis) and  
CC proliferative disorders. Antibodies, soluble proteins comprising  
CC extracellular domains and other regulators of B7-L polypeptides are  
CC useful for enhancing the immune response to tumours. (I) plays a role in  
CC growth and maintenance of cancer cells based on the observation of  
CC seminal vesicle hyperplasia in transgenic mice overexpressing B7-L  
CC polypeptide. Hence modulators of (I) are useful for the treatment of  
CC cancer including seminal vesicle cancer, lung, brain, breast, ovarian,  
CC testicular cancer and cancers of haematopoietic system. B7-L polypeptide  
CC pathway can be manipulated to regulate cytotoxic T-lymphocyte response in  
CC allograft transplantation, graft versus host disease, T-cell dependent B-  
CC cell mediated diseases and autoimmune diseases. B7-L molecules are useful  
CC for alleviating the symptoms associated with diseases involving chronic  
CC immune cell dysfunction or to treat autoimmune diseases such as systemic  
CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes,  
CC immune thrombocytopenic purpura and psoriasis, chronic inflammatory  
CC disease such as inflammatory bowel disease (Crohn's disease and  
CC ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and  
CC diabetes mellitus. They are also useful as immunosuppressive agents for  
CC bone marrow and organ transplantation or to prolong graft survival. B7-L  
CC molecules are also useful for diagnosis and treatment of diseases  
CC involving abnormal cell proliferation, including arteriosclerosis and  
CC vascular restenosis. Antagonists of B7-L polypeptides are useful for  
CC alleviation of toxic shock syndrome or all sensitisation due to blood  
CC transfusions, and for treatment of allergy, asthma and hypersensitivity  
CC reactions, nephropathies (e.g. glomerulonephritis), skin disorders  
CC (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various  
CC pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease,  
CC anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia  
CC gravis, and lymphoproliferative disorders such as multiple myeloma. The  
CC present sequence represents the coding sequence of human B7-L<sub>h3</sub>

SQ Sequence 1240 BP; 318 A; 319 C; 305 G; 298 T; 0 U; 0 Other;

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QY 61 AACCTGGTGGCTTAGAACATGGAAGGCAATTTGCTCACGGTTCCAGAACTGTAGGTT 120  
DB 61 AACCTGGTGGCTTAGAACATGGAAGGCAATTTGCTCACGGTTCCAGAACTGTAGGTT 120  
QY 121 TGGGTCTGGTAATGAAGTCTAGAACGCCGCCAGAAATGCAACAGTCTGAAGGGCTCCCA 180  
DB 121 TGGGTCTGGTAATGAAGTCTAGAACGCCGCCAGAAATGCAACAGTCTGAAGGGCTCCCA 180  
QY 181 GGCTCGCTTCAACTGCACCGCTCTCCAGAGGCTTGAAGCTCATCATGTGGGCTCTCAGTGA 240  
DB 181 GGCTCGCTTCAACTGCACCGCTCTCCAGAGGCTTGAAGCTCATCATGTGGGCTCTCAGTGA 240  
QY 241 CATGGTGGTCTAAGCGTCAAGGCCCATGGAGGCCCATCATCACCATGACCGCTTACCTC 300  
DB 241 CATGGTGGTCTAAGCGTCAAGGCCCATGGAGGCCCATCATCACCATGACCGCTTACCTC 300  
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QY 361 CAGTGATTCCGGGAACATCAGATCGACCTCCAGAACAGTCGCGCTCATGTGATCTGCTTA 420  
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QY 541 CTGGAGAGTCTGGCTCTCTGGTCTGAGCCATTCAGAGCTATTATTTGTTCCGAGCCACGCA 600  
DB 541 CTGGAGAGTCTGGCTCTCTGGTCTGAGCCATTCAGAGCTATTATTTGTTCCGAGCCACGCA 600  
QY 601 CTTTCAAATGTGAGTGAAGCATCTGGCTCTGACCCACAGAGCAATGGGACTTTGACTTG 660  
DB 601 CTTTCAAATGTGAGTGAAGCATCTGGCTCTGACCCACAGAGCAATGGGACTTTGACTTG 660  
QY 661 CTGGGTCTCTCGAGAGCTGAGGCCCGCGAGCTGCAACTGTAAATCTCACTGTGAT 720  
DB 661 CTGGGTCTCTCGAGAGCTGAGGCCCGCGAGCTGCAACTGTAAATCTCACTGTGAT 720  
QY 721 TCGGTCTCCCAAGACACCTGGAGGTGTTAATAATTCAGAGTGTATTATCAAGTTTACC 780  
DB 721 TCGGTCTCCCAAGACACCTGGAGGTGTTAATAATTCAGAGTGTATTATCAAGTTTACC 780  
QY 781 GAGTTAGGTTTTTTCATTCGCTACTTTGGGCGAAAGTTGCACTTGGACTAGCGGACCAT 840  
DB 781 GAGTTAGGTTTTTTCATTCGCTACTTTGGGCGAAAGTTGCACTTGGACTAGCGGACCAT 840  
QY 841 GCTTCTGAGCGCGAGCTGCTGCTGCTCTCTCAATAGCTGCTGCTGCGCGCTGTTGTTG 900  
DB 841 GCTTCTGAGCGCGAGCTGCTGCTGCTCTCTCAATAGCTGCTGCTGCGCGCTGTTGTTG 900  
QY 901 TGGCTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
DB 901 TGGCTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
QY 961 TCAATTTCAAAGAAATCTGAAAAGAGAGAAACAAAGAAAGAAAGAGAGTTGG 1020  
DB 961 TCAATTTCAAAGAAATCTGAAAAGAGAGAAACAAAGAAAGAAAGAGAGTTGG 1020  
QY 1021 AAATGAAACTCCGGCTACAAATTCAGATGAACAAAAGAGACCAAGAAACCGCTTCTCTCCC 1080  
DB 1021 AAATGAAACTCCGGCTACAAATTCAGATGAACAAAAGAGACCAAGAAACCGCTTCTCTCCC 1080  
QY 1081 TCCCAAATCCTGTGAATCCAGTGTATCTGAAACAAAGAAACAGTAGCTGTGGCCCTCTCTCA 1140  
DB 1081 TCCCAAATCCTGTGAATCCAGTGTATCTGAAACAAAGAAACAGTAGCTGTGGCCCTCTCTCA 1140  
QY 1141 CAGCGGGCTGTATCAAGCTCCAGCCAGGCGAGCAAGTCACTCCACAGGCTTCTTTTAACTCT 1200  
DB 1141 CAGCGGGCTGTATCAAGCTCCAGCCAGGCGAGCAAGTCACTCCACAGGCTTCTTTTAACTCT 1200  
QY 1201 GGCCAGTCTCTGAGAGGTCAAGTAATACTAGTAGTATAG 1240  
DB 1201 GGCCAGTCTCTGAGAGGTCAAGTAATACTAGTAGTATAG 1240

RESULT 2

ADB62950

ID ADB62950 standard; cDNA; 2051 BP.

XX ADB62950;

AC ADB62950;

DT 04-DEC-2003 (first entry)

XX Human cDNA encoding clone PLACE60177880.

DE Human; ss; gene; pharmaceutical; diagnostic; gene therapy;

XX tissue regeneration; cell regeneration; membrane protein;

KW signal transduction-related protein; transcription-related protein;

KW osteoporosis; neurological disease; cancer; tumour.

XX Homo sapiens.

OS

XX



XX Human; B7-Like protein; B7-L; antiinfertility; gynaecological;  
KW antitumor; cytostatic; immunosuppressive; antiarthritic; antirheumatic;  
KW antiinflammatory; dermatological; antipsoriatic; neuroprotective;  
KW antidiabetic; haemostatic; antichyroid; antitumor; antiallergic;  
KW antidiabetic; nephrotropic; antibacterial; virucide; tumour; cancer;  
KW reproductive disorder; graft versus host disease; autoimmune disease;  
KW toxic shock syndrome; allergy; nephropathy; skin disorder;  
KW endocrinopathy; lymphoproliferative disorder; gene; ss.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 27..1175  
FT FT /\*tag= a  
FT FT /product= "B7-Like protein, B7-L\_h1"  
XX  
FN WO200200710-A2.  
PD 03-JAN-2002.  
XX  
XX 28-JUN-2001; 2001WO-US020719.  
XX  
XX 28-JUN-2000; 2000US-0214512P.  
PR 28-NOV-2000; 2000US-00729264.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Welcher AA, Sarmiento UM, Schultz HJ, Chute HT;  
XX WPI; 2002-130881/17.  
DR P-PSDB; AAU75540.  
XX  
XX New B7-Like polypeptides, polynucleotides and their modulators, useful  
PT for diagnosing, preventing and treating reproductive, immune and  
PT proliferative disorders, e.g. cancer and arteriosclerosis.  
XX  
XX Claim 1; Fig 1; 135pp; English.  
XX  
XX The invention relates to an isolated B7-Like (B7-L) polypeptide (I). The  
CC polypeptide, polynucleotide encoding it and antibody against (I) are  
CC useful for treating B7-Like polypeptide-related disease, disorders or  
CC conditions including reproductive disorders (e.g. infertility,  
CC miscarriage, preterm labour and delivery and endometriosis) and  
CC proliferative disorders. Antibodies, soluble proteins comprising  
CC extracellular domains and other regulators of B7-L polypeptides are  
CC useful for enhancing the immune response to tumours. (I) plays a role in  
CC growth and maintenance of cancer cells based on the observation of  
CC seminal vesicle hyperplasia in transgenic mice overexpressing B7-L  
CC polypeptide. Hence modulators of (I) are useful for the treatment of  
CC cancer including seminal vesicle cancer, lung, brain, breast, ovarian,  
CC testicular cancer and cancers of haematopoietic system. B7-L polypeptide  
CC pathway can be manipulated to regulate cytotoxic T-lymphocyte response in  
CC allograft transplantation, graft versus host disease, T-cell dependent B-  
CC cell mediated diseases and autoimmune diseases. B7-L molecules are useful  
CC for alleviating the symptoms associated with diseases involving chronic  
CC immune cell dysfunction or to treat autoimmune diseases such as systemic  
CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes,  
CC immune thrombocytopenic purpura and psoriasis, chronic inflammatory  
CC disease such as inflammatory bowel disease (Crohn's disease and  
CC ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and  
CC diabetes mellitus. They are also useful as immunosuppressive agents for  
CC bone marrow and organ transplantation or to prolong graft survival. B7-L  
CC molecules are also useful for diagnosis and treatment of diseases  
CC involving abnormal cell proliferation, including arteriosclerosis and  
CC vascular stenosis. Antagonists of B7-L polypeptides are useful for  
CC alleviation of toxic shock syndrome or alloimmunisation due to blood  
CC transfusions, and for treatment of allergy, asthma and hypersensitivity  
CC reactions, nephropathies (e.g. glomerulonephritis), skin disorders  
CC (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various  
CC pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease,  
CC anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia  
CC gravis, and lymphoproliferative disorders such as multiple myeloma. The

CC present sequence represents the coding sequence of human B7-L\_h1  
XX  
SQ Sequence 1175 BP; 295 A; 307 C; 286 G; 287 T; 0 U; 0 Other;  
Query Match 86.6%; Score 1074; DB 6; Length 1175;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 116 GGTCTCTGGTCTGGTAATGAAGTCATAGAGGCCCCAGAGTCAACACAGTCTCTGAAGGCG 175  
DB 51 GGTCTCTGGTCTGGTAATGAAGTCATAGAGGCCCCAGAGTCAACACAGTCTCTGAAGGCG 110  
QY 176 TCCAGGCTCGCTTCAACTGCACCGCTCTCCAGGGCTGGAAGCTCATCATGTGGGCTCTC 235  
DB 111 TCCAGGCTCGCTTCAACTGCACCGCTCTCCAGGGCTGGAAGCTCATCATGTGGGCTCTC 170  
QY 236 AGTGACATGGTGGTCTAAGCGTCAGGCCCATGAGGCCCATCATCATCAATGACCGCTTC 295  
DB 171 AGTGACATGGTGGTCTAAGCGTCAGGCCCATGAGGCCCATCATCATCAATGACCGCTTC 230  
QY 296 ACTCTCTCAGAGGTACGACCCAGGGCGGGAATTCACCTCGGAGATGATCATCCACAATGTG 355  
DB 231 ACTCTCTCAGAGGTACGACCCAGGGCGGGAATTCACCTCGGAGATGATCATCCACAATGTG 290  
QY 356 GAGCCCATGATTTCGGGGAAATCATAGATCAGCGCTCCAGAACAGTCCGCTGCATGATCT 415  
DB 291 GAGCCCATGATTTCGGGGAAATCATAGATCAGCGCTCCAGAACAGTCCGCTGCATGATCT 350  
QY 416 GCTTACCTTACCGTCCAGTTATGGAGAGCTGTTCATTCACCGTCCAGTGTAACTTTAGTGC 475  
DB 351 GCTTACCTTACCGTCCAGTTATGGAGAGCTGTTCATTCACCGTCCAGTGTAACTTTAGTGC 410  
QY 476 GCTGAGAATGAACCTTTGTGAAGTTACTTCTTACCTCACAAGTGGACCGGCTCCCGGAT 535  
DB 411 GCTGAGAATGAACCTTTGTGAAGTTACTTCTTACCTCACAAGTGGACCGGCTCCCGGAT 470  
QY 536 ATTTCTGGAGCTCGGTCTCTGTGTCAGCCCAATCAAGCTATTAATTTTTCGGAGGCC 595  
DB 471 ATTTCTGGAGCTCGGTCTCTGTGTCAGCCCAATCAAGCTATTAATTTTTCGGAGGCC 530  
QY 596 ACGGACCTTCAAGTGCAGTGCAGTCTGAGTCTGAGCCCGACAGAGCAATGGGACTTTG 655  
DB 531 ACGGACCTTCAAGTGCAGTGCAGTCTGAGTCTGAGCCCGACAGAGCAATGGGACTTTG 590  
QY 656 ACTTGTGCTGCTTACCTTGAAGAGCTTGAAGGCCGCAAGTCTGCAACTGTAAATCTCACT 715  
DB 591 ACTTGTGCTGCTTACCTTGAAGAGCTTGAAGGCCGCAAGTCTGCAACTGTAAATCTCACT 650  
QY 716 GTGATTTCGGTGTCCCAAGACACTGGAGTGGTATTAAATTAATTCAGGTGTATTATCAAGT 775  
DB 651 GTGATTTCGGTGTCCCAAGACACTGGAGTGGTATTAAATTAATTCAGGTGTATTATCAAGT 710  
QY 776 TTACCGAGTTTAGTGTTCATTCGCTACTTGGGGCAAGTTGGACTTGGACTAGCAGGC 835  
DB 711 TTACCGAGTTTAGTGTTCATTCGCTACTTGGGGCAAGTTGGACTTGGACTAGCAGGC 770  
QY 836 ACCATGCTTCTCAGCCCGACGTGACTCTTACAATACGCTGTCTGTGCTGCGCCGCTCGT 895  
DB 771 ACCATGCTTCTCAGCCCGACGTGACTCTTACAATACGCTGTCTGTGCTGCGCCGCTCGT 830  
QY 896 TGTGTGGTGTCAACTGTGCTGCGGTTGTGTTTCTGTGTAGAGAAAAAGAGATT 955  
DB 831 TGTGTGGTGTCAACTGTGCTGCGGTTGTGTTTCTGTGTAGAGAAAAAGAGATT 890  
QY 956 CGTATTCAATTTCAAGGAAATCTGAAGAGAGAGACAAACAAGAACTGACAGAA 1015  
DB 891 CGTATTCAATTTCAAGGAAATCTGAAGAGAGAGACAAACAAGAACTGACAGAA 950  
QY 1016 AGTGAAATGAAATCTCCGGCTTACAAATTCAGATGAACAAAGACCAAGAAACCGCTTCT 1075  
DB 951 AGTGAAATGAAATCTCCGGCTTACAAATTCAGATGAACAAAGACCAAGAAACCGCTTCT 1010  
QY 1076 CTCCTCCCAATCTGTGAATCCAGTGTCTGAACAAAGAAACAGTAGTGTGGCCCT 1135

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Db      1011  CTCCTCCCAATCTGTGTAATCAGTGATCTCTGAACAAAGAAACAGTAGCTGTGGCCCT 1070
QY      1136  CCTCACCAGCGGCTGTATCAAGCTCCACCCAGCCAGCAAGTCATCCACAGGCTTCTTTT 1195
Db      1071  CCTCACCAGCGGCTGTATCAAGCTCCACCCAGCCAGCAAGTCATCCACAGGCTTCTTTT 1130
QY      1196  AATCTGCCAGTCTCTGAGAAGGTCAGTAATACAACTGTAGTATAG 1240
Db      1131  AATCTGCCAGTCTCTGAGAAGGTCAGTAATACAACTGTAGTATAG 1175

RESULT 4
ABK13029
ID  ABK13029 standard; cDNA; 1168 BP.
XX
AC  ABK13029;
XX
DT  23-APR-2002 (first entry)
XX
DE  DNA encoding human B7-like protein, B7-L_h2.
XX
KW  Human; B7-like protein; B7-L; antiinfertility; gynaecological;
KW  antitumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic;
KW  antiinflammatory; dermatological; antipsoriatic; neuroprotective;
KW  antidiabetic; haemostatic; antithyroid; antiulcer; antiallergic;
KW  antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer;
KW  reproductive disorder; graft versus host disease; autoimmune disease;
KW  toxic shock syndrome; allergy; nephropathy; skin disorder;
KW  endocrinopathy; lymphoproliferative disorder; gene; ss.
XX
OS  Homo sapiens.
XX
FH  Key      Location/Qualifiers
FT  CDS      8..1168
FT  /tag= a
FT  /product= "B7-like protein, B7-L_h2"
XX
WO200200710-A2.
XX
PD  03-JAN-2002.
XX
PF  28-JUN-2001; 2001WO-US020719.
XX
PR  28-JUN-2000; 2000US-0214512P.
XX
PR  28-NOV-2000; 2000US-00729264.
XX
XX  (AMGE-) AMGEN INC.
XX
PI  Welcher AA, Sarmiento UM, Schultz HJ, Chute HT;
XX
DR  WPI; 2002-130881/17.
XX
DR  P-PSDB; AAU75541.
XX
XX  New B7-like polypeptides, polynucleotides and their modulators, useful
XX  for diagnosing, preventing and treating reproductive, immune and
XX  proliferative disorders, e.g. cancer and arteriosclerosis.
XX
PS  Claim 1; Fig 2; 135pp; English.
XX
XX  The invention relates to an isolated B7-like (B7-L) polypeptide (I). The
XX  polypeptide, polynucleotide encoding it and antibody against (I) are
XX  useful for treating B7-like polypeptide-related disease, disorders or
XX  conditions including reproductive disorders (e.g. infertility,
XX  miscarriage, preterm labour and delivery and endometriosis) and
XX  proliferative disorders. Antibodies, soluble proteins comprising
XX  extracellular domains and other regulators of B7-L polypeptides are
XX  useful for enhancing the immune response to tumours. (I) plays a role in
XX  growth and maintenance of cancer cells based on the observation of
XX  seminal vesicle hyperplasia in transgenic mice overexpressing B7-L
XX  polypeptide. Hence modulators of (I) are useful for the treatment of
XX  cancer including seminal vesicle cancer, lung, brain, breast, ovarian,
XX  testicular cancer and cancers of haematopoietic system. B7-L polypeptide

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CC  pathway can be manipulated to regulate cytotoxic T-lymphocyte response in
CC  allograft transplantation, graft versus host disease, T-cell dependent B-
CC  cell mediated diseases and autoimmune diseases. B7-L molecules are useful
CC  for alleviating the symptoms associated with diseases involving chronic
CC  immune cell dysfunction or to treat autoimmune diseases such as systemic
CC  lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes,
CC  immune thrombocytopenic purpura and psoriasis, chronic inflammatory
CC  disease such as inflammatory bowel disease (Crohn's disease and
CC  ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and
CC  diabetes mellitus. They are also useful as immunosuppressive agents for
CC  bone marrow and organ transplantation or to prolong graft survival. B7-L
CC  molecules are also useful for diagnosis and treatment of diseases
CC  involving abnormal cell proliferation, including arteriosclerosis and
CC  vascular restenosis. Antagonists of B7-L polypeptides are useful for
CC  alleviation of toxic shock syndrome or allosensitisation due to blood
CC  transfusions, and for treatment of allergy, asthma and hypersensitivity
CC  reactions, nephropathies (e.g. glomerulonephritis), skin disorders
CC  (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various
CC  pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease,
CC  anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia
CC  gravis, and lymphoproliferative disorders such as multiple myeloma. The
CC  present sequence represents the coding sequence of human B7-L_h2
XX
SQ  Sequence 1168 BP; 299 A; 302 C; 288 G; 279 T; 0 U; 0 Other;
      Query Match      78.7%; Score 976; DB 6; Length 1168;
      Best Local Similarity 99.8%; Pred. No. 0;
      Matches 1076; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY  163  AGTCCTGAAGGGCTCCAGGCTCGCTTCAACTGCACCGTCTCCAGGGCTGGAAGTCTCAT 222
      |||||
Db  91  AGTCCTGAAGGGCTCCAGGCTCGCTTCAACTGCACCGTCTCCAGGGCTGGAAGTCTCAT 150
QY  223  CATGTGGGCTCTCAGTGACATGTGTGCTGAAGCGTCAGGCCCATGAGGCCCATCATCAC 282
      |||||
Db  151  CATGTGGGCTCTCAGTGACATGTGTGCTGAAGCGTCAGGCCCATGAGGCCCATCATCAC 210
QY  283  CAATGACCGCTTCACCTCTCAGAGGTACGACACGAGGGGGAACTTCACTCGGAGATGAT 342
      |||||
Db  211  CAATGACCGCTTCACCTCTCAGAGGTACGACACGAGGGGGAACTTCACTCGGAGATGAT 270
QY  343  CATCCACAATGTGGAGCCAGTGATTCGGGGAAACATCAGATGACGCTCCAGCAACAGTCG 402
      |||||
Db  271  CATCCACAATGTGGAGCCAGTGATTCGGGGAAACATCAGATGACGCTCCAGCAACAGTCG 330
QY  403  CTTGCATGGAATCTGCTTACCTTACCGTCCAAAGTTATGGGAGAGCTGTTCAATCCAGTGT 462
      |||||
Db  331  CTTGCATGGAATCTGCTTACCTTACCGTCCAAAGTTATGGGAGAGCTGTTCAATCCAGTGT 390
QY  463  TAATCTTGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCTCAGCTGGAC 522
      |||||
Db  391  TAATCTTGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCTCAGCTGGAC 450
QY  523  CCGGCTCCCGGATATTTCTCTGGAGCTCGGTCTCTCTGGTCAGCCATTCAAGCTATTATTT 582
      |||||
Db  451  CTGGCTCCCGGATATTTCTCTGGAGCTCGGTCTCTCTGGTCAGCCATTCAAGCTATTATTT 510
QY  583  TGTTCGGAGCCCGAGCGACCTTCAAAGTCAGTGAGATCTCTGGCTCTGACCCACAGAG 642
      |||||
Db  511  TGTTCGGAGCCCGAGCGACCTTCAAAGTCAGTGAGATCTCTGGCTCTGACCCACAGAG 570
QY  643  CAATGGAGCTTTGACATTCGGTGGCTACCTCGGAGAGCCTGAAGCCCGGAAAGTCTCAAC 702
      |||||
Db  571  CAATGGAGCTTTGACATTCGGTGGCTACCTCGGAGAGCCTGAAGCCCGGAAAGTCTCAAC 630
QY  703  TGTAAATCTCACGTGATTCGGTGTCTCCCAAGACACTGGAGGTGGTATTAAATATTCAGG 762
      |||||
Db  631  TGTAAATCTCACGTGATTCGGTGTCTCCCAAGACACTGGAGGTGGTATTAAATATTCAGG 690
QY  763  TGTATTATCAAGTTTACCGAGTTTAGTGTTCATTTCCCTACTTGGGGCAAGTGTGACT 822
      |||||
Db  691  TGTATTATCAAGTTTACCGAGTTTAGTGTTCATTTCCCTACTTGGGGCAAGTGTGACT 750

```

QY 823 TGGACTAGCAGCACCATTCTTCTGACGCCGCGTGTACTCTTACAATACGCTGCTGCTG 882  
Db |||  
751 TGGACTAGCAGCACCATTCTTCTGACGCCGCGTGTACTCTTACAATACGCTGCTGCTG 810  
QY 883 CTGCGCGCTCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 942  
Db |||  
811 CTGCGCGCTCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 870  
QY 943 AAAAGAGGATTTCTGTTTCAATTTCAAAAGAAATCTGAAAAGAGAGACAAACAAAGA 1002  
Db |||  
871 AAAAGAGGATTTCTGTTTCAATTTCAAAAGAAATCTGAAAAGAGAGACAAACAAAGA 930  
QY 1003 AACTGAGACAGAAAGTGAATGAAATCTCGGCTACAATCTCAGATGAACAAAGACAC 1062  
Db |||  
931 AACTGAGACAGAAAGTGAATGAAATCTCGGCTACAATCTCAGATGAACAAAGACAC 990  
QY 1063 AGAAACCGCTTCTCTCCCTCCCAATCTGAAATCTGAAATCTGAAATCTGAAATCTGAA 1122  
Db |||  
991 AGACACCGCTTCTCTCCCTCCCAATCTGAAATCTGAAATCTGAAATCTGAAATCTGAA 1050  
QY 1123 TAGCTGTGCGCTCTCTCCCTCCCAATCTGAAATCTGAAATCTGAAATCTGAAATCTGAA 1182  
Db |||  
1051 TAGCTGTGCGCTCTCTCCCTCCCAATCTGAAATCTGAAATCTGAAATCTGAAATCTGAA 1110  
QY 1183 ACAGGCTTCTTTAATCTGCGCAGTCTCTGAGAGGTGAGTAACTGATAGTAGTAGTAG 1240  
Db |||  
1111 ACAGGCTTCTTTAATCTGCGCAGTCTCTGAGAGGTGAGTAACTGATAGTAGTAGTAG 1168

RESULT 5

ID ABK13031

ABK13031 standard; cdNA; 1139 BP.

AC ABK13031;

DT 23-APR-2002 (first entry)

XX DNA encoding human B7-like protein, B7-L<sub>h4</sub>.

XX Human; B7-like protein; B7-L; antiinfertility; gynaecological;  
KW antitumor; cytostatic; immunosuppressive; antiarthritic; antirheumatic;  
KW antinflammatory; dermatological; antipsoriatic; neuroprotective;  
KW antidiabetic; haemostatic; antithyroid; antitumor; antiallergic;  
KW antiasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer;  
KW reproductive disorder; graft versus host disease; autoimmune disease;  
KW toxic shock syndrome; allergy; nephropathy; skin disorder;  
KW endocrinopathy; lymphoproliferative disorder; gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers  
FH 1. .1134  
FT /\*tag= a  
FT /product= "B7-like protein, B7-L<sub>h4</sub>"

XX WO200200710-A2.

XX 03-JAN-2002.

XX 28-JUN-2001; 2001WO-US020719.

XX 28-JUN-2000; 2000US-0214512P.

XX 28-NOV-2000; 2000US-00729264.

XX (AMGE-) AMGEN INC.

XX Welcher AA, Sarmiento UM, Schultz HJ, Chute HT;

XX WPI; 2002-130881/17.

XX New B7-like polypeptides, polynucleotides and their modulators, useful  
PT for diagnosing, preventing and treating reproductive, immune and  
PT proliferative disorders, e.g. cancer and arteriosclerosis.

Claim 1; Fig 4; 135pb; English.

XX The invention relates to an isolated B7-like (B7-L) polypeptide (I). The  
XX polypeptide, polynucleotide encoding it and antibody against (I) are  
XX useful for treating B7-like polypeptide-related disease, disorders or  
XX conditions including reproductive disorders (e.g. infertility),  
XX miscarriage, preterm labour and delivery and endometriosis) and  
XX proliferative disorders. Antibodies, soluble proteins comprising  
XX extracellular domains and other regulators of B7-L polypeptides are  
XX useful for enhancing the immune response to tumours. (I) plays a role in  
XX growth and maintenance of cancer cells based on the observation of  
XX seminal vesicle hyperplasia in transgenic mice overexpressing B7-L  
XX polypeptide. Hence modulators of (I) are useful for the treatment of  
XX cancer including seminal vesicle cancer, lung, brain, breast, ovarian,  
XX testicular cancer and cancers of haematopoietic system. B7-L polypeptide  
XX pathway can be manipulated to regulate cytotoxic T-lymphocyte response in  
XX allograft transplantation, graft versus host disease, T-cell dependent B-  
XX cell mediated diseases and autoimmune diseases. B7-L molecules are useful  
XX for alleviating the symptoms associated with diseases involving chronic  
XX immune cell dysfunction or to treat autoimmune diseases such as systemic  
XX lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes,  
XX immune thrombocytopenic purpura and psoriasis, chronic inflammatory  
XX disease such as inflammatory bowel disease (Crohn's disease and  
XX ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and  
XX diabetes mellitus. They are also useful as immunosuppressive agents for  
XX bone marrow and organ transplantation or to prolong graft survival. B7-L  
XX molecules are also useful for diagnosis and treatment of diseases  
XX involving abnormal cell proliferation, including arteriosclerosis and  
XX vascular stenosis. Antagonists of B7-L polypeptides are useful for  
XX alleviation of toxic shock syndrome or alloensitisation due to blood  
XX transfusions, and for treatment of allergy, asthma and hypersensitivity  
XX reactions, nephropathies (e.g. glomerulonephritis), skin disorders  
XX (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various  
XX pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease,  
XX anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia  
XX gravis, and lymphoproliferative disorders such as multiple myeloma. The  
XX present sequence represents the coding sequence of human B7-L<sub>h4</sub>

SQ Sequence 1139 BP; 290 A; 300 C; 283 G; 266 T; 0 U; 0 Other;

Query Match 59.6%; Score 739; DB 6; Length 1139;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 789; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 163 AGTCCTGAAGGGCTCCAGGCTCGCTTCAACTGACCGCTCTCCAGGGCTGGAAGTCAT 222

Db |||

84 AGTCCTGAAGGGCTCCAGGCTCGCTTCAACTGACCGCTCTCCAGGGCTGGAAGTCAT 143

QY 223 CATGTGGGCTCTCAGTGACATGGTGTCTAAGCGGTGAGGCCCATCGAGCCCATCATC 282

Db |||

144 CATGTGGGCTCTCAGTGACATGGTGTCTAAGCGGTGAGGCCCATCGAGCCCATCATC 203

QY 283 CAATGACCGCTTCACTCTCAGAGTACGACCGGGGGGAACTTCACTCCGAGATGAT 342

Db |||

204 CAATGACCGCTTCACTCTCAGAGTACGACCGGGGGGAACTTCACTCCGAGATGAT 263

QY 343 CATCCCAATGTGGAGCCCGAGTGATTCGGGGAAACATCAGATGAGCCTCCAGAACAGTCG 402

Db |||

264 CATCCCAATGTGGAGCCCGAGTGATTCGGGGAAACATCAGATGAGCCTCCAGAACAGTCG 323

QY 403 CTGCAATGGATCTGCTTACCTTACCGTCCAAGTTATGGAGAGCTGTTTCATTCGCCAGTGT 462

Db |||

324 CTGCAATGGATCTGCTTACCTTACCGTCCAAGTTATGGAGAGCTGTTTCATTCGCCAGTGT 383

QY 463 TAACTTTGTAGTCGCTGAGAAATGACCTTGTGAAGTTACTTGTCTACCTCCACATGGAC 522

Db |||

384 TAACTTTGTAGTCGCTGAGAAATGACCTTGTGAAGTTACTTGTCTACCTCCACATGGAC 443

QY 523 CCGGCTCCCGGATATTTCTCTGGAGCTCGGTCTCTCTGGTCCAGCATTTCAAGCTATTATTT 582

Db |||

444 CCGGCTCCCGGATATTTCTCTGGAGCTCGGTCTCTCTGGTCCAGCATTTCAAGCTATTATTT 503





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RESULT 7
ACH16130
ID ACH16130 standard; cDNA; 474 BP.
XX
AC ACH16130;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human adult heart cDNA #444.
XX
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
OS Homo sapiens.
XX
XX US2003073623-A1.
PN
PD
XX 17-APR-2003.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
PI
XX WPI; 2003-615964/58.
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 3342; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
XX Sequence 474 BP; 154 A; 128 C; 96 G; 95 T; 0 U; 1 Other;
SQ
Query Match 21.6%; Score 268; DB 8; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.4e-124;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 973 GAAATCTGAAAAGACAGAGCAACAAAGAACTGAGACAGAAAGTGGAAATGAAACTC 1032
DB 63 GAAATCTGAAAAGACAGAGCAACAAAGAACTGAGACAGAAAGTGGAAATGAAACTC 122
QY 1033 CGGCTCAATTGAGTGAACAAAGAACCCAGAGAACCGCTTCTCCCTCCCAAAATCCCTG 1092
DB 123 CGGCTCAATTGAGTGAACAAAGAACCCAGAGAACCGCTTCTCCCTCCCAAAATCCCTG 182

QY 1093 TGAATCCAGTGATCTCTGAACAAAGAAACAGTAGCTGTGGCCCTCTCCACAGCGGCTGA 1152
DB 183 TGAATCCAGTGATCTCTGAACAAAGAAACAGTAGCTGTGGCCCTCTCCACAGCGGCTGA 242
QY 1153 TCAAGCTCCACCCAGCGCAGCAAGTCATCCACAGGCTTCTTTTAATCTGGCCAGTCTCTGA 1212
DB 243 TCAAGCTCCACCCAGCGCAGCAAGTCATCCACAGGCTTCTTTTAATCTGGCCAGTCTCTGA 302
QY 1213 GAAGGTCAGTAATACAACTGTAGTATAG 1240
DB 303 GAAGGTCAGTAATACAACTGTAGTATAG 330

RESULT 8
AAI36582
ID AAI36582 standard; DNA; 401 BP.
XX
AC AAI36582;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #5268 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
OS Homo sapiens.
XX
XX WO200157272-A2.
PN
PD
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX Claim 25; SEQ ID NO 5268; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders
XX
XX Sequence 401 BP; 105 A; 98 C; 111 G; 87 T; 0 U; 0 Other;
SQ
Query Match 11.6%; Score 144; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.7e-62;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 AGTCCTGAAGGGCTCCAGGCTCGCTTCAACTGCACCGTCTCCAGGGCTGGAGCTCAT 222
DB 258 AGTCCTGAAGGGCTCCAGGCTCGCTTCAACTGCACCGTCTCCAGGGCTGGAGCTCAT 317
QY 223 CATGTGGGCTCTCAGTGACATGGTGTGCTTAAGCGCTCAGGCCCATGAGCCCATCATCAC 282
DB 318 CATGTGGGCTCTCAGTGACATGGTGTGCTTAAGCGCTCAGGCCCATGAGCCCATCATCAC 377
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QY 283 CAATGACCGCTTCACTCTCAGAG 306  
 Db 378 CAATGACCGCTTCACTCTCAGAG 401

RESULT 9  
 AAI04335  
 ID AAI04335 standard; DNA; 357 BP.  
 XX AAI04335;  
 XX 09-OCT-2001 (first entry)  
 XX  
 DE Probe #4326 used to measure gene expression in human breast sample.  
 XX  
 XX Probe; human; breast disease; breast cancer; development disorder; ss;  
 KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157270-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 XX 29-JAN-2001; 2001WO-US000661.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-476286/51.  
 XX  
 PT Novel single exon nucleic acid probe used to measuring gene expression in  
 PT a human breast.  
 XX  
 PS Claim 25; SEQ ID NO 4326; 322pp; English.  
 XX  
 CC The present invention relates to novel single exon nucleic acid probes.  
 CC The present sequence is one such probe. The probes are useful for  
 CC measuring human gene expression in a human breast sample, where the probe  
 CC hybridises at high stringency to a nucleic acid expressed in the human  
 CC breast. The probes are useful for predicting, diagnosing, grading,  
 CC staging, monitoring and prognosing diseases of the human breast,  
 CC particularly those diseases with polygenic aetiology. The diseases  
 CC include: breast cancer, disorders of development, inflammatory diseases  
 CC of the breast, fibrocystic changes, proliferative breast disease and non-  
 CC carcinoma tumours. Note: The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 357 BP; 117 A; 68 C; 64 G; 108 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 25; DB 5; Length 357;  
 Best Local Similarity 100.0%; Pred. No. 0.069;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 949 AGGATTTCGATTCAATTCAAAG 973  
 Db 42 AGGATTTCGATTCAATTCAAAG 66

RESULT 10  
 ABL15493/c  
 ID ABL15493 standard; cDNA; 6507 BP.

XX ABL15493;  
 AC  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40961.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ss.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 XX 23-MAR-2001; 2001WO-US009231.  
 PF  
 XX  
 XX 23-MAR-2000; 2000US-0191637P.  
 PR  
 PR 11-JUL-2000; 2000US-00614150.  
 XX  
 XX (PEKE ) PE CORP NY.  
 PA  
 XX  
 XX Venter JC, Adams M, Li PWD, Myers EW;  
 PI  
 XX  
 DR WPI; 2001-656860/75.  
 DR P-PSDB; ABB71390.  
 XX  
 XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signaling and cell-cell  
 PT interactions.  
 XX  
 PS Claim 1; SEQ ID NO 40961; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABU16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABR57737-  
 CC ABR72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 6507 BP; 1745 A; 1888 C; 1712 G; 1162 T; 0 U; 0 Other;  
 Query Match 1.9%; Score 24; DB 4; Length 6507;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 872 CGCTGCTGCTGCTGCCGCGCTCGT 895  
 Db 2946 CGCTGCTGCTGCTGCCGCGCTCGT 2923

RESULT 11  
 ABL15492/c  
 ID ABL15492 standard; cDNA; 59967 BP.  
 XX  
 AC ABL15492;  
 XX  
 XX 26-MAR-2002 (first entry)  
 DT  
 XX  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40958.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ss.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX

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PD 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
PR
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
DR
XX P-PSDB; ABB711389.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
XX Claim 1; SEQ ID NO 40958; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 59967 BP; 17305 A; 12463 C; 12291 G; 17908 T; 0 U; 0 Other;
SQ
Query Match 1.9%; Score 24; DB 4; Length 59967;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 872 CGTGTGCTGCTGCGCGCGTGT 895
DB 4596 CGCTGCTGCTGCTGCGCGTGT 4573
RESULT 12
ID ABL13032
XX ABL13032 standard; cDNA; 1195 BP.
XX
XX ABL13032;
XX
XX 23-APR-2002 (first entry)
XX
XX DNA encoding mouse B7-like protein, B7-L_m1.
XX
XX Mouse; B7-like protein; B7-L; antiinfertility; gynaecological;
XX antitumour; cytostatic; immunosuppressive; antiarthritic; antirheumatic;
XX antiinflammatory; dermatological; antipsoriatic; neuroprotective;
XX antidiabetic; haemostatic; antithyroid; antitumor; antiallergic;
XX antasthmatic; nephrotropic; antibacterial; virucide; tumour; cancer;
XX reproductive disorder; graft versus host disease; autoimmune disease;
XX toxic shock syndrome; allergy; nephropathy; skin disorder;
XX endocrinopathy; lymphoproliferative disorder; gene; ss.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 53..1165
XX /*tag= a
XX /product= "B7-like protein, B7-L_m1"
XX
XX WO200200710-A2.
XX
XX 03-JAN-2002.
XX
XX 28-JUN-2001; 2001WO-US020719.

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XX 28-JUN-2000; 2000US-0214512P.
PR
XX 28-NOV-2000; 2000US-00729264.
XX
XX (AMGE-) AMGEN INC.
XX
XX Welcher AA, Sarmiento UM, Schultz HJ, Chute HT;
XX
XX WPI; 2002-130881/17.
DR
XX P-PSDB; AAU75544.
XX
XX New B7-like polypeptides, polynucleotides and their modulators, useful
PT for diagnosing, preventing and treating reproductive, immune and
PT proliferative disorders, e.g. cancer and arteriosclerosis.
XX
XX Claim 1; Fig 5; 135pp; English.
XX
XX The invention relates to an isolated B7-like (B7-L) polypeptide (I). The
CC polypeptide, polynucleotide encoding it and antibody against (I) are
CC useful for treating B7-like polypeptide-related disease, disorders or
CC conditions including reproductive disorders (e.g. infertility,
CC miscarriage, preterm labour and delivery and endometriosis) and
CC proliferative disorders. Antibodies, soluble proteins comprising
CC extracellular domains and other regulators of B7-L polypeptides are
CC useful for enhancing the immune response to tumours. (I) plays a role in
CC growth and maintenance of cancer cells based on the observation of
CC seminal vesicle hyperplasia in transgenic mice overexpressing B7-L
CC polypeptide. Hence modulators of (I) are useful for the treatment of
CC cancer including seminal vesicle cancer, lung, brain, breast, ovarian,
CC testicular cancer and cancers of haematopoietic system. B7-L polypeptide
CC pathway can be manipulated to regulate cytotoxic T-lymphocyte response in
CC allograft transplantation, graft versus host disease, T-cell dependent B-
CC cell mediated diseases and autoimmune diseases. B7-L molecules are useful
CC for alleviating the symptoms associated with diseases involving chronic
CC immune cell dysfunction or to treat autoimmune diseases such as systemic
CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis, diabetes,
CC immune thrombocytopenic purpura and psoriasis, chronic inflammatory
CC disease such as inflammatory bowel disease (Crohn's disease and
CC ulcerative colitis), Grave's disease, Hashimoto's thyroiditis and
CC diabetes mellitus. They are also useful as immunosuppressive agents for
CC bone marrow and organ transplantation or to prolong graft survival. B7-L
CC molecules are also useful for diagnosis and treatment of diseases
CC involving abnormal cell proliferation, including arteriosclerosis and
CC vascular restenosis. Antagonists of B7-L polypeptides are useful for
CC alleviation of toxic shock syndrome or allosensitisation due to blood
CC transfusions, and for treatment of allergy, asthma and hypersensitivity
CC reactions, nephropathies (e.g. glomerulonephritis), skin disorders
CC (pemphigus and pemphigoid), endocrinopathies (Grave's disease), various
CC pneumopathies (extrinsic alveolitis), vasculopathies, coeliac disease,
CC anaemia, thrombocytopenias, Guillain-Barre syndrome and myasthenia
CC gravis, and lymphoproliferative disorders such as multiple myeloma. The
CC present sequence represents the coding sequence of mouse B7-L_m1
XX
XX Sequence 1195 BP; 313 A; 304 C; 291 G; 287 T; 0 U; 0 Other;
SQ
Query Match 1.9%; Score 23; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 527 CTCCTCGGATATTCTCTGGAGCT 549
DB 521 CTCCTCGGATATTCTCTGGAGCT 543
RESULT 13
AAV99359
XX AAV99359 standard; DNA; 141 BP.
XX
XX AAV99359;
XX
XX 25-MAR-1999 (first entry)
XX
XX 5' PCR primer for GDNFR-gammal cDNA encoding the full length protein.

```

XX Glial cell line-derived neurotrophic factor receptor gamma 1;  
 KW GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;  
 KW neurodegenerative disease; anyotrophic lateral sclerosis; GDNFR-gamma1;  
 KW Parkinson's disease; schizophrenia; insomnia; tardive dyskinesia;  
 KW hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;  
 KW renal disorder; kidney failure; gut dysfunction; regeneration;  
 KW cardiomyocyte; epithelium; hepatocyte; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX WO9853069-A2.  
 XX  
 PD 26-NOV-1998.  
 XX  
 XX 20-MAY-1998; 98WO-US010328.  
 PF  
 XX 20-MAY-1997; 97US-0047092P.  
 PR  
 PR 27-JUN-1997; 97US-00884638.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX  
 XX Ni J, Hsu T, Young P, Gentz RL, Ruben SM;  
 PI WPI; 1999-070150/06.  
 XX  
 DR New isolated glial cell derived neurotrophic factor receptors - used to  
 PT develop products for treating e.g. neurodegenerative disorders,  
 PT schizophrenia, hypertension, tumours, renal disorders, kidney failure or  
 PT gut dysfunction.  
 XX  
 XX Example 6; Page 68; 156pp; English.  
 PS  
 XX PCR primers AAV99359-60 were used to amplify cDNA encoding the full  
 CC length protein of a glial cell line-derived neurotrophic factor receptor  
 CC gamma 1 (GDNFR-gamma1). The amplified product was subsequently cloned and  
 CC expressed in Baculovirus. GDNFR-beta shares high homology with GDNFR-  
 CC alpha, which is capable of complexing with glial cell line-derived  
 CC neurotrophic factor (GDNF) and mediating cell response to GDNF. The GDNFR  
 CC polypeptides and agonists can be used for treating disorders associated  
 CC with decreased activity of the respective polypeptides. They can be used  
 CC for treating neurodegenerative diseases such as amyotrophic lateral  
 CC sclerosis, Parkinson's disease, schizophrenia, insomnia, tardive  
 CC dyskinesia, hypertension, pituitary adenomas, hyperprolactinemia, thyroid  
 CC tumour, renal disorders, kidney failure, gut dysfunction, or for  
 CC regeneration of cardiomyocytes, epithelium or hepatocytes. Antagonists of  
 CC the polypeptides can be used for treating disorders associated with  
 CC increased activity of the respective polypeptides. The products can also  
 CC be used for detection, diagnosis and drug screening  
 XX  
 SQ Sequence 141 BP; 19 A; 60 C; 38 G; 24 T; 0 U; 0 Other;  
 Query Match 1.8%; Score 22; DB 2; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 2.2;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 873 GCTGCTGCTGCTGCCGCCGCG 894  
 Db 69 GCTGCTGCTGCTGCCGCCGCG 90  
 RESULT 14  
 ABN99162  
 XX ID ABN99162 standard; DNA; 767 BP.  
 AC  
 XX ABN99162;  
 XX  
 DT 01-AUG-2002 (first entry)  
 XX  
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 930.  
 XX  
 XX Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;  
 KW

KW disease; crop; thale cress; tolerance factor; insect; pathogen;  
 KW nutrition; ds.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN US2002023281-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 XX 26-JAN-2001; 2001US-00770445.  
 PF  
 XX 27-JAN-2000; 2000US-0178472P.  
 PR  
 XX (GORL/) GORLACH J.  
 PA (ANY/) AN Y.  
 PA (HAML/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (RAIN/) RAINES T M.  
 PA (YUYV/) YU Y.  
 PA (RAME/) RAMEAKA J G.  
 PA (PAGE/) PAGE A.  
 PA (MATH/) MATHW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.  
 PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.  
 PA (KRICK/) KRICKER M.  
 PA (SLAT/) SLATER T.  
 PA (DAVI/) DAVIS K R.  
 PA (ALLE/) ALLEN K.  
 PA (HOFF/) HOFFMAN N.  
 PA (HURB/) HURBAN P.  
 XX  
 XX Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;  
 PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;  
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;  
 PI Hurban P;  
 XX  
 XX WPI; 2002-403163/43.  
 XX New Arabidopsis thaliana nucleic acid for identifying homologous genes,  
 PT producing compositions that modulate the expression or function of its  
 PT encoded protein, and mapping functional regions of protein.  
 XX  
 PS Claim 1; SEQ ID NO 930; 49pp + Sequence Listing; English.  
 CC The invention relates to an Arabidopsis thaliana nucleic acid (I)  
 CC comprising a sequence capable of hybridising under stringent conditions  
 CC to a sequence selected from any one of 999 sequences (ABN98233-ABN99231),  
 CC given in the specification or its fragment. A polypeptide (II) encoded by  
 CC (I), a transgenic plant (III) comprising an exogenous nucleic acid or a  
 CC genetically modified cell (IV) comprising an exogenous nucleic acid, is  
 CC useful for screening a candidate agent for its biological effect. (I) is  
 CC useful in identifying homologous or related genes, in producing  
 CC compositions that modulate the expression or function of its encoded  
 CC protein, mapping functional regions of the protein and in studying  
 CC associated physiological pathways. (I) is also useful for the genetic  
 CC manipulation of cells, particularly plant cells. (I) is also useful in  
 CC screening assays of various plant strains to determine the strains that  
 CC are best capable of withstanding a particular disease or environmental  
 CC stress. (II) and (III) are useful for screening of biologically active  
 CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical  
 CC pathways. The screened agents are useful in improved methods of treating  
 CC crops to prevent or treat disease. (II) are also useful in screening  
 CC programs to identify agents that mimic or enhance the action of tolerance  
 CC factors. Such agents are useful in improved methods of treating crops to  
 CC enhance their tolerance to environmental stress. (I) is also useful for  
 CC enhancing or inhibiting production of a biosynthetic product in a plant.  
 CC (III) is useful for identifying other mediators that may induce  
 CC expression of proteins of interest, for establishing the extent to which  
 CC any specific insect and/or pathogen is responsible for damage to a  
 CC particular plant, for identifying other mediators that enhance or induce  
 CC tolerance to environmental stress, for identifying factors involved in

CC biosynthetic pathways of nutritional, commercial, or medicinal value and  
 CC for identifying productions of nutritional, commercial or medicinal  
 CC value. (IV) is useful in the study of genetic function and regulation,  
 CC for alteration of the cellular metabolism and for screening compounds  
 CC that may affect the biological function of the gene or gene products.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from USPTO  
 CC at seqdata.uspto.gov/sequence.html?DocID=999909770445

XX Sequence 767 BP; 169 A; 199 C; 147 G; 252 T; 0 U; 0 Other;  
 SQ Query Match 1.8%; Score 22; DB 6; Length 767;  
 Best Local Similarity 100.0%; Pred. No. 2.3;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 886 CGCCGCTGCTTGTGCTGC 907  
 DB 672 CGCCGCTGCTTGTGCTGC 693

RESULT 15  
 AAV35364  
 ID AAV35364 standard; cDNA; 1200 BP.  
 XX AC AAV35364;  
 XX DT 28-SEP-1998 (first entry)  
 XX DE Human GDNF alpha-3 receptor cDNA #1.  
 XX KW Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;  
 KW treatment; neurodegenerative disease; Parkinson's Disease; ALS; SMA;  
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;  
 KW Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;  
 KW muscular dystrophy; diagnostic; ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT CDS 1..1200  
 FT /\*tag= a  
 FT /product= "GDNF alpha-3"  
 FT /notes= "partial sequence of glial cell-derived  
 FT neurotrophic factor alpha-3 receptor"

XX EP846764-A2.  
 XX PD 10-JUN-1998.  
 XX PF 20-NOV-1997; 97EP-00309375.  
 XX PR 27-NOV-1996; 96GB-00024677.  
 XX PR 09-MAY-1997; 97GB-00009463.  
 XX PA (SMIX ) SMITHKLINE BEECHAM PLC.  
 XX PI Lawrence GMP;  
 XX WPI; 1998-299980/27.  
 XX F-PSDB; AAW65116.  
 XX PT New factor alpha 3 receptor polypeptide and e.g. DNA and agonists - used  
 XX to treat neuro degenerative diseases, muscular diseases and nerve and  
 XX muscle trauma and in diagnostic assays.  
 XX PS Claim 9; Fig 1; 22pp; English.  
 XX CC This sequence encodes a novel glial cell line-derived neurotrophic factor  
 CC alpha-3 receptor (GDNF alpha-3). This protein can be used to treat e.g.  
 CC neurodegenerative diseases (such as Parkinson's Disease, amyotrophic  
 CC lateral sclerosis (ALS), spinal muscular atrophy (SMA), Huntington's  
 CC Disease, Alzheimer's Disease, diabetic neuropathy), muscular diseases  
 CC (including the muscular dystrophies) and nerve and muscle trauma and in

CC diagnostic assays for such conditions  
 XX SQ Sequence 1200 BP; 236 A; 419 C; 307 G; 238 T; 0 U; 0 Other;  
 Query Match 1.8%; Score 22; DB 2; Length 1200;  
 Best Local Similarity 100.0%; Pred. No. 2.3;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 873 GCTGCTGCTGCTGCCGCTGC 894  
 DB 51 GCTGCTGCTGCTGCCGCTGC 72

Search completed: September 14, 2004, 23:41:50  
 Job time : 533.923 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	22	1.8	1203	3	US-09-220-528-65	Sequence 65, Appl
2	22	1.8	1699	4	US-09-187-906-20	Sequence 20, Appl
3	22	1.8	3942	3	US-09-162-484-19	Sequence 19, Appl
C 4	21	1.7	550	4	US-09-669-751-128	Sequence 128, Appl
C 5	21	1.7	1428	4	US-09-489-039A-3243	Sequence 3243, Appl
6	20	1.6	394	4	US-09-621-976-16752	Sequence 16752, A
7	20	1.6	794	4	US-09-621-976-16751	Sequence 16751, A
8	20	1.6	984	4	US-09-252-991A-12897	Sequence 12897, A
9	20	1.6	1857	4	US-09-252-991A-12897	Sequence 12897, A
C 10	20	1.6	1910	3	US-09-593-711A-3	Sequence 3, Appl
C 11	20	1.6	1914	1	US-07-601-094-1	Sequence 1, Appl
C 12	20	1.6	1914	1	US-07-601-735-1	Sequence 1, Appl
13	20	1.6	2214	3	US-08-864-038A-1	Sequence 1, Appl
14	20	1.6	3331	3	US-08-864-038A-2	Sequence 2, Appl
15	20	1.6	3331	3	US-08-864-038A-4	Sequence 4, Appl
16	20	1.6	6407	2	US-08-616-844-7	Sequence 7, Appl
17	20	1.6	6407	2	US-08-599-654-7	Sequence 7, Appl
18	20	1.6	6407	3	US-08-944-868A-7	Sequence 7, Appl
19	20	1.6	6407	3	US-08-944-423A-7	Sequence 7, Appl
20	20	1.6	6407	3	US-08-944-496-7	Sequence 7, Appl
C 21	19	1.5	402	4	US-09-621-976-88	Sequence 88, Appl
C 22	19	1.5	1425	1	US-08-464-148-1	Sequence 1, Appl
C 23	19	1.5	1425	1	US-08-385-500-1	Sequence 1, Appl
C 24	19	1.5	1425	1	US-08-846-784-1	Sequence 1, Appl
C 25	19	1.5	1477	4	US-09-620-312D-1019	Sequence 1019, Appl
C 26	19	1.5	1768	4	US-09-833-381-523	Sequence 523, Appl
27	19	1.5	1899	4	US-09-919-060-15	Sequence 15, Appl

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/187,906  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/07726  
FILING DATE: 07-MAY-97  
APPLICATION NUMBER: US 60/017,427  
FILING DATE: 08-MAY-96  
APPLICATION DATA: US 60/019,300  
FILING DATE: 07-JUN-96  
APPLICATION DATA: US 60/021,859  
FILING DATE: 16-JUL-96  
APPLICATION DATA: US 60/043,533  
FILING DATE: 10-APR-97  
ATTORNEY/AGENT INFORMATION:  
NAME: Kaplan, Warren A.  
REGISTRATION NUMBER: 34,199  
REFERENCE/DOCKET NUMBER: A008 PCT CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-679-2400  
TELEFAX: 617-679-2838  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1699 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 175..1374  
US-09-187-906-20

Query Match 1.8%; Score 22; DB 4; Length 1699;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 873 GCTGCTGCTGCTGCCCGCTCG 894  
Db 225 GCTGCTGCTGCTGCCCGCTCG 246  
RESULT 3  
US-09-162-484-19  
; Sequence 19, Application US/09162484  
; Patent No. 6248724  
; GENERAL INFORMATION:  
; APPLICANT: Phillips, M. Ian  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS TARGETED TO  
; FILE REFERENCE: UFLA:087/UFLA087P  
; CURRENT APPLICATION NUMBER: US/09/162,484  
; CURRENT FILING DATE: 1998-09-25  
; EARLIER APPLICATION NUMBER: 60/059,661  
; EARLIER FILING DATE: 1997-09-25  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 3942  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-09-162-484-19

Query Match 1.8%; Score 22; DB 3; Length 3942;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 873 GCTGCTGCTGCTGCCCGCTCG 894  
Db 72 GCTGCTGCTGCTGCCCGCTCG 93  
RESULT 4  
US-09-669-751-128/c  
; Sequence 128, Application US/09669751  
; Patent No. 6551575  
; GENERAL INFORMATION:  
; APPLICANT: Greenspan, Ralph J.  
; TITLE OF INVENTION: Methods for Identifying Compounds for  
; TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to  
; TITLE OF INVENTION: Balance and the Perception of Gravity  
; FILE REFERENCE: P-NI 3864  
; CURRENT APPLICATION NUMBER: US/09/669,751  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 60/168,579  
; PRIOR FILING DATE: 1999-12-02  
; NUMBER OF SEQ ID NOS: 261  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 128  
; LENGTH: 550  
; TYPE: DNA  
; ORGANISM: Drosophila  
US-09-669-751-128

Query Match 1.7%; Score 21; DB 4; Length 550;  
Best Local Similarity 100.0%; Pred. No. 0.56;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 909 ACTGCTGCTGCCGTGTGTT 929  
Db 317 ACTGCTGCTGCCGTGTGTT 297

RESULT 5  
US-09-489-039A-3243/c  
; Sequence 3243, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 3243  
; LENGTH: 1428  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-3243

Query Match 1.7%; Score 21; DB 4; Length 1428;  
Best Local Similarity 100.0%; Pred. No. 0.59;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 186 GCTTCAACTGCACCGTCTCCC 206  
Db 1147 GCTTCAACTGCACCGTCTCCC 1127

RESULT 6  
US-09-621-976-16752  
; Sequence 16752, Application US/09621976  
; Patent No. 6639063

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; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 16752
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-16752

Query Match      1.6%; Score 20; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      882 GCTGCCGCCGCTGCTGTGT 901
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Db      34 GCTGCCGCCGCTGCTGTGT 53

RESULT 7
US-09-621-976-16751
; Sequence 16751, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 16751
; LENGTH: 794
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-16751

Query Match      1.6%; Score 20; DB 4; Length 794;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      882 GCTGCCGCCGCTGCTGTGT 901
        |||
Db      34 GCTGCCGCCGCTGCTGTGT 53

US-09-252-991A-12897
; ORGANISM: Pseudomonas aeruginosa
; Sequence 12735, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12735
; LENGTH: 1857
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12735

Query Match      1.6%; Score 20; DB 4; Length 1857;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      899 TGTGGCTGCAACTGCTGCTG 918
        |||
Db      1746 TGTGGCTGCAACTGCTGCTG 1765

RESULT 9
US-09-252-991A-12735
; Sequence 12735, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12735
; LENGTH: 1857
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12735

Query Match      1.6%; Score 20; DB 4; Length 1857;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      899 TGTGGCTGCAACTGCTGCTG 918
        |||
Db      1746 TGTGGCTGCAACTGCTGCTG 1765

RESULT 10
US-09-593-711A-3/c
; Sequence 3, Application US/09593711A
; Patent No. 6271030
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
; FILE REFERENCE: RTS-0118
; CURRENT APPLICATION NUMBER: US/09/593,711A
; CURRENT FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 244
; SEQ ID NO 3
; LENGTH: 1910
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
; NAME/KEY: unsure
; LOCATION: 1415
; NAME/KEY: unsure
; LOCATION: 1421
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 1422
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 1423
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OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 1424  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 1458  
OTHER INFORMATION: unknown  
NAME/KEY: CDS  
LOCATION: (299)...(1336)  
US-09-593-711A-3

Query Match 1.6%; Score 20; DB 3; Length 1910;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 872 CGCTGCTGCTGCTGCCGCG 891  
DB 205 CGCTGCTGCTGCTGCCGCG 186

RESULT 11  
US-07-601-094-1/c  
Sequence 1, Application US/07601094  
Patent No. 5215892  
GENERAL INFORMATION:  
APPLICANT: Kishimoto, Tadamitsu  
APPLICANT: Hirano, Toshio  
APPLICANT: Akira, Shizuo  
APPLICANT: Ishiki, Hiroshi  
APPLICANT: Tanabe, Osamu  
APPLICANT: Kinoshita, Shigemi  
APPLICANT: Shimamoto, Takuya  
TITLE OF INVENTION: C/BBP2 Gene and Recombinant  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak &  
ADDRESS: Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/601,094  
FILING DATE: 19901022  
CLASSIFICATION: 435  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1914 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 281..1316  
OTHER INFORMATION:  
US-07-601-094-1

Query Match 1.6%; Score 20; DB 1; Length 1914;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 872 CGCTGCTGCTGCTGCCGCG 891  
DB 204 CGCTGCTGCTGCTGCCGCG 185

RESULT 12  
US-08-012-735-1/c  
Sequence 1, Application US/08012735  
Patent No. 5360894  
GENERAL INFORMATION:  
APPLICANT: Kishimoto, Tadamitsu  
APPLICANT: Hirano, Toshio  
APPLICANT: Akira, Shizuo  
APPLICANT: Ishiki, Hiroshi  
APPLICANT: Tanabe, Osamu  
APPLICANT: Kinoshita, Shigemi  
APPLICANT: Shimamoto, Takuya  
TITLE OF INVENTION: C/BBP2 Gene and Recombinant  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak &  
ADDRESS: Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/012,735  
FILING DATE: 19930203  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/601,094  
FILING DATE: 22 OCT 1990  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1914 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 281..1316  
OTHER INFORMATION:  
US-08-012-735-1

Query Match 1.6%; Score 20; DB 1; Length 1914;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 872 CGCTGCTGCTGCTGCCGCG 891  
DB 204 CGCTGCTGCTGCTGCCGCG 185

RESULT 13  
US-08-864-038A-1  
Sequence 1, Application US/08864038A  
Patent No. 6001592  
GENERAL INFORMATION:  
APPLICANT: Kunio NAKASHIMA et al.  
TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE cDNA, VECTOR



```
; TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
; TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
; TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
; TITLE OF INVENTION: TO SAID POLYPEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: 812-5 Hirano
; STREET: Isshinden
; CITY: Tsu-city
; STATE: Mie-prefecture
; COUNTRY: JAPAN
; ZIP: 514-01
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Word Perfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,038A
; FILING DATE: May 28, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-184459
; FILING DATE: 15-July-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: C. Bruce Hamburg
; REGISTRATION NUMBER: 22,389
; REFERENCE/DOCKET NUMBER: F-5610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)986-2340
; TELEFAX: (212)953-7733
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2214
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Pinctada fucata
; CELL TYPE: mantle epithelial cell
; US-08-864-038A-1
;
Query Match 1.6%; Score 20; DB 3; Length 2214;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 872 CGCTGCTGCTGCTGCCGCCG 891
Db 855 CGCTGCTGCTGCTGCCGCCG 874

RESULT 14
US-08-864-038A-2
; Sequence 2, Application US/08864038A
; Patent No. 6001592
; GENERAL INFORMATION:
; APPLICANT: Kunio NAKASHIMA et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
; TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
; TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
; TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: 812-5 Hirano
; STREET: Isshinden
; CITY: Tsu-city
; STATE: Mie-prefecture
; COUNTRY: JAPAN
; ZIP: 514-01
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Word Perfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,038A
; FILING DATE: May 28, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-184459
; FILING DATE: 15-July-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: C. Bruce Hamburg
; REGISTRATION NUMBER: 22,389
; REFERENCE/DOCKET NUMBER: F-5610
; TELECOMMUNICATION INFORMATION:
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; SOFTWARE: Word Perfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,038A
; FILING DATE: May 28, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-184459
; FILING DATE: 15-July-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: C. Bruce Hamburg
; REGISTRATION NUMBER: 22,389
; REFERENCE/DOCKET NUMBER: F-5610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)986-2340
; TELEFAX: (212)953-7733
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3331
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Pinctada fucata
; CELL TYPE: mantle epithelial cell
; FEATURE: mRNA
; LOCATION: from 1 to 3331
; IDENTIFICATION METHOD: E (by experiment)
; US-08-864-038A-2
;
Query Match 1.6%; Score 20; DB 3; Length 3331;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 872 CGCTGCTGCTGCTGCCGCCG 891
Db 904 CGCTGCTGCTGCTGCCGCCG 923

RESULT 15
US-08-864-038A-4
; Sequence 4, Application US/08864038A
; Patent No. 6001592
; GENERAL INFORMATION:
; APPLICANT: Kunio NAKASHIMA et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
; TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
; TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
; TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: 812-5 Hirano
; STREET: Isshinden
; CITY: Tsu-city
; STATE: Mie-prefecture
; COUNTRY: JAPAN
; ZIP: 514-01
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Word Perfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,038A
; FILING DATE: May 28, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-184459
; FILING DATE: 15-July-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: C. Bruce Hamburg
; REGISTRATION NUMBER: 22,389
; REFERENCE/DOCKET NUMBER: F-5610
; TELECOMMUNICATION INFORMATION:
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; TELEPHONE: (212)986-2340
; TELEFAX: (212)953-7733
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 3331
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA to mRNA
;   ORIGINAL SOURCE: Pinctada fucata
;   ORGANISM: Pinctada fucata
;   CELL TYPE: mantle epithelial cell
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: from 50 to 2263
;     IDENTIFICATION METHOD: P (by similarity to some other pattern)
US-08-864-038A-4
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Query Match      1.6%; Score 20; DB 3; Length 3331;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      872 CGCTGCTGCTGCTGCCGCCG 891
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Db       904 CGCTGCTGCTGCTGCCGCCG 923
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OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 23:16:34 ; Search time 658.934 Seconds  
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Perfect score: 1240  
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7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq: \*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq: \*  
9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq: \*  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq: \*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq: \*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq: \*  
13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq: \*  
14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq: \*  
15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq: \*  
16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq: \*  
17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq: \*  
18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq: \*  
19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1125	90.7	2051	16	US-10-104-047-1104
2	268	21.6	474	10	US-09-918-995-3342
3	144	11.6	401	9	US-09-864-761-16305
4	25	2.0	357	9	US-09-864-761-16653
5	24	1.9	1078	13	US-10-027-632-255100
6	24	1.9	1078	13	US-10-027-632-255101
7	24	1.9	1078	13	US-10-027-632-255102
8	24	1.9	1078	16	US-10-027-632-255100
9	24	1.9	1078	16	US-10-027-632-255101
10	24	1.9	1078	16	US-10-027-632-255102
11	24	1.9	1121	13	US-10-027-632-257899
12	24	1.9	1121	16	US-10-027-632-257899
13	23	1.9	1284	17	US-10-437-963-81852
14	22	1.8	767	9	US-09-770-445-930

15	1.8	1203	9	US-09-220-920-65	Sequence 65, Appl
16	1.8	1829	9	US-09-828-366-15	Sequence 15, Appl
17	1.8	4142	12	US-10-152-319A-1498	Sequence 1498, Ap
18	1.8	4571	9	US-09-764-847-1043	Sequence 1043, Ap
19	1.8	4571	15	US-10-092-154-1043	Sequence 1043, Ap
20	1.8	10462	9	US-09-764-847-1044	Sequence 1044, Ap
21	1.8	10462	10	US-09-764-891-6203	Sequence 6203, Ap
22	1.8	10462	15	US-10-092-154-1044	Sequence 1044, Ap
23	1.7	462	17	US-10-437-963-41506	Sequence 41506, A
24	1.7	493	10	US-09-918-995-11051	Sequence 11051, A
25	1.7	550	15	US-10-255-536-128	Sequence 128, App
26	1.7	602	17	US-10-767-701-28842	Sequence 28842, A
27	1.7	606	13	US-10-027-632-134169	Sequence 134169, A
28	1.7	606	16	US-10-027-632-134169	Sequence 134169, A
29	1.7	645	13	US-10-027-632-285369	Sequence 285369, A
30	1.7	645	13	US-10-027-632-285370	Sequence 285370, A
31	1.7	645	16	US-10-027-632-285369	Sequence 285369, A
32	1.7	645	16	US-10-027-632-285370	Sequence 285370, A
33	1.7	1558	10	US-09-930-213-20	Sequence 20, Appl
34	1.7	3362	13	US-10-087-192-185	Sequence 185, App
35	1.7	94917	13	US-10-087-192-184	Sequence 184, App
36	1.7	357652	17	US-10-322-696-34	Sequence 34, Appl
37	1.6	330	17	US-10-437-963-55684	Sequence 55684, A
38	1.6	358	13	US-09-823-245A-58	Sequence 58, Appl
39	1.6	398	9	US-09-983-965-4945	Sequence 4945, Ap
40	1.6	412	10	US-09-918-995-5855	Sequence 5855, Ap
41	1.6	442	13	US-10-027-632-320734	Sequence 320734, A
42	1.6	442	16	US-10-027-632-320734	Sequence 320734, A
43	1.6	507	17	US-10-430-201-970	Sequence 970, App
44	1.6	507	17	US-10-430-201-971	Sequence 971, App
45	1.6	596	17	US-10-767-701-5378	Sequence 5378, Ap

ALIGNMENTS

RESULT 1  
US-10-104-047-1104  
; Sequence 1104, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20030236392a1el full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1104  
; LENGTH: 2051  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-104-047-1104

Query Match	90.7%	Score 1125;	DB 16;	Length 2051;
Best Local Similarity	100.0%	Pred. No. 0;	Mismatches 0;	Indels 0;
Matches 1125;	Conservative 0;			Gaps 0;
QY	116	GGTTCGGGTCTCGTAAATGAAGTCATAGAAGGCCCCAGAAATGCAACAGTCTCTGAAGGC	175	
Db	203	GGTTCGGGTCTCGTAAATGAAGTCATAGAAGGCCCCAGAAATGCAACAGTCTCTGAAGGC	262	
QY	176	TCCAGGCTCGTTCACCTGACCGTCTCCAGGGTGGAGCTCATATGTGGGTCTC	235	
Db	263	TCCAGGCTCGTTCACCTGACCGTCTCCAGGGTGGAGCTCATATGTGGGTCTC	322	
QY	236	AGTGACATGGTGGTCTAGCGTCAGGCCCATGAGCCCATCATCCATGACCGGCTTC	295	
Db	323	AGTGACATGGTGGTCTAGCGTCAGGCCCATGAGCCCATCATCCATGACCGGCTTC	382	
QY	296	ACCTCTCAGAGGTACGACCGAGGGCGGAACTTCACCTCGGAGATGATCATCCACAATGTG	355	

Db 383 ACCTCTCAGAGTACGACGAGCGGGAACCTTCCACCTCGAGATGATCATCCACAATGTG 442  
QY 356 GAGCCAGGATTCGGGGAACTCAGATCAGCTCCAGACAGTGCCTGATGATCT 415  
Db 443 GAGCCAGGATTCGGGGAACTCAGATCAGCTCCAGACAGTGCCTGATGATCT 502  
QY 416 GCTTACCTTACCGTCCAAAGTATGGAGAGCTGTTTCATTCACAGTGTAAATCTGTAGTC 475  
Db 503 GCTTACCTTACCGTCCAAAGTATGGAGAGCTGTTTCATTCACAGTGTAAATCTGTAGTC 562  
QY 476 GCTGAGAAATGAACTTGTGAAGTACTTGTCTACCTCAGCTGAGACCGCGTCCCGGAT 535  
Db 563 GCTGAGAAATGAACTTGTGAAGTACTTGTCTACCTCAGCTGAGACCGCGTCCCGGAT 622  
QY 536 ATTTCCTGGAGCTCGGTCTCCTGTCAGCCATTCAGCTATTAATTTCTCCGAGCCC 595  
Db 623 ATTTCCTGGAGCTCGGTCTCCTGTCAGCCATTCAGCTATTAATTTCTCCGAGCCC 682  
QY 596 AGCGACCTTCAAAGTGCAGTGAGCATCTCGGTCTGACCCACAGACCAATGGGACTTTG 655  
Db 683 AGCGACCTTCAAAGTGCAGTGAGCATCTCGGTCTGACCCACAGACCAATGGGACTTTG 742  
QY 656 ACTTGGTGGCTACCTGGAAGAGCTGAAGCCCGCAAGTCTGCAACTGTAAATCTCACT 715  
Db 743 ACTTGGTGGCTACCTGGAAGAGCTGAAGCCCGCAAGTCTGCAACTGTAAATCTCACT 802  
QY 716 GTGATTCGGTGTCCCCAAGACACTGGAGTGTGTTAATTAATTCAGCTGTTATCAAGT 775  
Db 803 GTGATTCGGTGTCCCCAAGACACTGGAGTGTGTTAATTAATTCAGCTGTTATCAAGT 862  
QY 776 TTACCGAGTTAGTTTTTCAITGGCTACTTGGGCAAGTTGGACTTGGACTAGCAGC 835  
Db 863 TTACCGAGTTAGTTTTTCAITGGCTACTTGGGCAAGTTGGACTTGGACTAGCAGC 922  
QY 836 ACATGCTTCTGAGCGGAGCTGTACTCTTAATAGCTGTCTGTGCTGCGCGCTGT 895  
Db 923 ACCATGCTTCTGAGCGGAGCTGTACTCTTAATAGCTGTCTGTGCTGCGCGCTGT 982  
QY 896 TGTGTGGCTGCAACTGCTGCTGCGCTGTGTTTCTGTGTAGAGAAAGAGGATTT 955  
Db 983 TGTGTGGCTGCAACTGCTGCTGCGCTGTGTTTCTGTGTAGAGAAAGAGGATTT 1042  
QY 956 CATTATCAATTTCAAAGAAATCTGAAAAGAGAGACAAACAAAGAACTGAGACAGAA 1015  
Db 1043 CGTATTCATTTCAAAGAAATCTGAAAAGAGAGACAAACAAAGAACTGAGACAGAA 1102  
QY 1016 AGTGAATGAAATCTCCGGCTACATTCAGATGAACAAAGACCAACAGACCGCTTCT 1075  
Db 1103 AGTGAATGAAATCTCCGGCTACATTCAGATGAACAAAGACCAACAGACCGCTTCT 1162  
QY 1076 CTCCCTCCCAATCTGTGAATCCAGTGATCTGAAACAAAGAAACAGTAGTGTGCGCT 1135  
Db 1163 CTCCCTCCCAATCTGTGAATCCAGTGATCTGAAACAAAGAAACAGTAGTGTGCGCT 1222  
QY 1136 CTTCCACGCGGCTGATCAACGTCACCCAGCAGCAAGTCAATCCACAGGCTTCTTTT 1195  
Db 1223 CTTCCACGCGGCTGATCAACGTCACCCAGCAGCAAGTCAATCCACAGGCTTCTTTT 1282  
QY 1196 AATCTGGCCAGCTCTGAGAGCTCAGTAATCAACTGTAGTATAG 1240  
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RESULT 2

US-09-918-995-3342  
; Sequence 3342, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FROM VARIOUS CDNA LIBRARIES  
; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 3342  
; LENGTH: 474  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)...(474)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-3342

Query Match 21.6%; Score 268; DB 10; Length 474;  
Best Local Similarity 100.0%; Pred. No. 3.5e-129;  
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 973 GAAATCTGAAAAGAGAGACAAACAAAGAACTGAGACAGAAAGTGAATAATGAAACTC 1032  
Db 63 GAAATCTGAAAAGAGAGACAAACAAAGAACTGAGACAGAAAGTGAATAATGAAACTC 122  
QY 1033 CGGCTACAAATTCAGATGAACAAAGAACCAACAGAAACCGCTTCTCTCCCTCCCAATCCTG 1092  
Db 123 CGGCTACAAATTCAGATGAACAAAGAACCAACAGAAACCGCTTCTCTCCCTCCCAATCCTG 182  
QY 1093 TGAATCCAGTGTCTGAAACAAAGAAACAGTAGTGTGCGCTCTCACCAGCGGCTGA 1152  
Db 183 TGAATCCAGTGTCTGAAACAAAGAAACAGTAGTGTGCGCTCTCACCAGCGGCTGA 242  
QY 1153 TCAACGCTCCACCGCAGCAGCAAGTCATCCACAGGCTTCTTTAATCTGCCAGTCCCTGA 1212  
Db 243 TCAACGCTCCACCGCAGCAGCAAGTCATCCACAGGCTTCTTTAATCTGCCAGTCCCTGA 302  
QY 1213 GAAGTCTAGTAATACAACTGTAGTATAG 1240  
Db 303 GAAGTCTAGTAATACAACTGTAGTATAG 330

RESULT 3

US-09-864-761-16305  
; Sequence 16305, Application US/09864761  
; Patent No. US2002048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aeonica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16305
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF1211782.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
; US-09-864-761-16305

Query Match      11.6%; Score 144; DB 9; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.4e-64;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 AGTCCTGAAGGCTCCAGGCTCGCTCACTGACCGTCTCCAGGCTGGAGCTCAT 222
DB 258 AGTCCTGAAGGCTCCAGGCTCGCTCACTGACCGTCTCCAGGCTGGAGCTCAT 317
QY 223 CATGTGGGCTCTCAGTGACATGTGTGTGTAAGCGTCCAGCCCATGAGCCCATCATCAC 282
DB 318 CATGTGGGCTCTCAGTGACATGTGTGTGTAAGCGTCCAGCCCATGAGCCCATCATCAC 377
QY 283 CAATGACCGCTTCACCTCTCAGAG 306
DB 378 CAATGACCGCTTCACCTCTCAGAG 401

RESULT 4
; US-09-864-761-16653
; Sequence 16653, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16653
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF064857.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.93
; US-09-864-761-16653

Query Match      2.0%; Score 25; DB 9; Length 357;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 949 AGGATTTTCGTATTCAATTTCAAAAG 973
DB 42 AGGATTTTCGTATTCAATTTCAAAAG 66

RESULT 5
; US-10-027-632-255100
; Sequence 255100, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 255100
; LENGTH: 1078
; TYPE: DNA
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; ORGANISM: Human
US-10-027-632-255100

Query Match
Best Local Similarity 1.9%; Score 24; DB 13; Length 1078;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 AGTTTCCTAGGCTGCCATAACAAA 53
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Db 871 AGTTTCCTAGGCTGCCATAACAAA 894

RESULT 6
US-10-027-632-255101
; Sequence 255101, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 255101
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-255101

Query Match
Best Local Similarity 1.9%; Score 24; DB 13; Length 1078;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 AGTTTCCTAGGCTGCCATAACAAA 53
    |||||
Db 871 AGTTTCCTAGGCTGCCATAACAAA 894

RESULT 7
US-10-027-632-255102
; Sequence 255102, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
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; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 255102
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-255102

Query Match
Best Local Similarity 1.9%; Score 24; DB 13; Length 1078;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 AGTTTCCTAGGCTGCCATAACAAA 53
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Db 871 AGTTTCCTAGGCTGCCATAACAAA 894

RESULT 8
US-10-027-632-255100
; Sequence 255100, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 255100
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-255100

Query Match
Best Local Similarity 1.9%; Score 24; DB 16; Length 1078;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 AGTTTCCTAGGCTGCCATAACAAA 53
    |||||
Db 871 AGTTTCCTAGGCTGCCATAACAAA 894

RESULT 9
US-10-027-632-255101
; Sequence 255101, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
```

FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 255101  
; LENGTH: 1078  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-255101

Query Match 1.9%; Score 24; DB 16; Length 1078;  
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;  
Matches 24; Conservative 0; Mismatches 0;

QY 30 AGTTCTAGGCTGCCATACAAA 53  
|||||  
Db 871 AGTTCTAGGCTGCCATACAAA 894

## RESULT 10

US-10-027-632-255102  
; Sequence 255102, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; POLYMERASE: Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 255102

; LENGTH: 1078

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-255102

Query Match 1.9%; Score 24; DB 16; Length 1078;  
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;  
Matches 24; Conservative 0; Mismatches 0;

QY 30 AGTTCTAGGCTGCCATACAAA 53  
|||||

Db 871 AGTTCTAGGCTGCCATACAAA 894

## RESULT 11

US-10-027-632-257899  
; Sequence 257899, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; POLYMERASE: Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 257899

; LENGTH: 1121

; TYPE: DNA

; ORGANISM: Human

; NAME/KEY: misc feature

; LOCATION: (1)...(1121)

; OTHER INFORMATION: n = A,T,C or G

US-10-027-632-257899

Query Match 1.9%; Score 24; DB 13; Length 1121;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 AGTTCTAGGCTGCCATACAAA 53  
|||||  
Db 915 AGTTCTAGGCTGCCATACAAA 938

## RESULT 12

US-10-027-632-257899  
; Sequence 257899, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; POLYMERASE: Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

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; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 257899
; LENGTH: 1121
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(1121)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-257899

Query Match
Best Local Similarity 1.9%; Score 24; DB 16; Length 1121;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 AGTTTCCTAGGTCGCATACAAA 53
DB 915 AGTTTCCTAGGTCGCATACAAA 938

RESULT 13
US-10-437-963-81852/c
; Sequence 81852, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 81852
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_81337C.1
US-10-437-963-81852

Query Match
Best Local Similarity 1.9%; Score 23; DB 17; Length 1284;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 872 CGCTGCTGCTGTCGCGCGCTGC 894
DB 156 CGCTGCTGCTGTCGCGCGCTGC 134

RESULT 14
US-09-770-445-930
; Sequence 930, Application US/09770445
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
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; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kriker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 930
; LENGTH: 767
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-930

Query Match
Best Local Similarity 1.8%; Score 22; DB 9; Length 767;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 886 CCGCGCTGCTGTTGTTGGCTGC 907
DB 672 CCGCGCTGCTGTTGTTGGCTGC 693

RESULT 15
US-09-220-920-65
; Sequence 65, Application US/09220920
; Patent No. US2002002269A1
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Baloh, Robert H.
; TITLE OF INVENTION: Artemin, A No. US20020002269A1el Neurotrophic Factor
; FILE REFERENCE: 6029-7996
; CURRENT APPLICATION NUMBER: US/09/220,920
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-920-65

Query Match
Best Local Similarity 1.8%; Score 22; DB 9; Length 1203;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 873 GCTGCTGCTGCTGCGCGCTGC 894
DB 51 GCTGCTGCTGCTGCGCGCTGC 72

Search completed: September 15, 2004, 07:20:17
Job time : 659.934 secs
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